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- GRAY SCALE DOCUMENTS

## IMAGES ARE BEST AVAILABLE COPY.

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APPLICANT: Mata, John B.
TITLE OF INVENTION: Syntheic Oligodeoxyribonucleotides
TITLE OF INVENTION: Which Mimic Telomeric Sequences for ITILE OF INVENTION: of Cancer and Other Diseases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zarely, McKee, Thomte, Voorhees, & Sease
STREET: 801 Grand Suite 3200
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,097A
             US-08-192-300-18

US-08-531-743-10

US-08-631-743-10

US-08-838-545-11

US-08-838-545-11

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US-08-838-545-21

US-08-838-545-21

US-08-949-532-11

US-09-349-532-11

US-09-349-532-17

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US-09-349-532-29
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APPLICATION UNBER: US/08/381,097A
FILLING DATE: 31-JAN.1995
CLASSIFICATION: 514
ATTORNEY, AGENT INPORMATION:
NAWE: NED-1, Heid is
REGISTRATION NUMBER: 37,719
REFERENCE/DOCKET NUMBER: unmc 63092
TELECOMUNICATION INFORMATION:
TELEPHONE: 515-288-3667
TELEPHONE: 515-288-3667
TELEPHONE: 515-288-3667
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 base pairs
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STATE: Iowa
COUNTRY: United States
71P: 50309
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STRANDEDNESS: single
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Sequence 9,
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(cgn2_6/ptodata/1/ina/5A_COMB.seq:*

(cgn2_6/ptodata/1/ina/5B_COMB.seq:*

(cgn2_6/ptodata/1/ina/6A_COMB.seq:*

(cgn2_6/ptodata/1/ina/6B_COMB.seq:*

(cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

(cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Gapop 10.0, uaptor ...

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Searched: 569978 seqs, 220691566 residues

Grotal number of hits satisfying chosen parameters:

Animum DB seq length: 0

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Gost-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries
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US-08-381-097A-5

US-08-151-097A-5

US-08-151-477A-4

US-08-151-477A-4

US-08-151-477A-4

US-08-151-477A-4

US-08-151-477A-4

US-08-199-3

US-08-199-3

US-09-1018-545-3

US-09-1018-545-3

US-09-378-535-9

US-09-378-535-9

US-09-378-535-9

US-09-378-535-9

US-09-378-535-9

US-08-838-545-35

US-08-838-545-35

US-08-838-545-36

US-09-349-532-34

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US-08-338-545-34

US-09-349-532-34

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Gapop 10.0 , Gapext 1.0
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Perfect score:
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Gaps
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THERAPY AND DIAGNOSIS OF CONDITIONS RELATED TO TELEOMERE LENGTH AND/OR TELOMERASE ACTIVITY
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| Patent No. 5686306
| GENERAL INFORMATION:
| APPLICANT: West, Michael David APPLICANT: Shay, Jerry APPLICANT: Wright, Woodring E. TITLE OF INVENTION: METHODS AND REAGENTS FOR TITLE OF INVENTION: METHODS AND REAGENTS OF SEQUENCES:
| TITLE OF INVENTION: METHODS AND RESERVED INVENTION: MEASURING TELOMERES INVENTION: MEASURING TELOMERES IN THE OF INVENTION OF INVENTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 810x896
COMPUTER: 1BM Compatible COMPUTER: 1BM COMPATION 1.5
CURRENT APPLICATION DATA: 845966cmber 12, 1993
PRIOR APPLICATION NUMBER: 08/038,766
FILING DATE: MARCH 24, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32, 327
REFERENCE/DOCKET NUMBER: 204/195
TELECOMMINICATION INFORMATION:
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 8torage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
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STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                               E: Lyon & Lyon
633 West Fifth Street
Suite 4700
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Best Local Similarity 100.0
The Green Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
   TITLE OF INVENTION: THER TITLE OF INVENTION: CONUTITLE OF INVENTION: LENGURBER OF SEQUENCES: 58 CORRESPONDENCE ADDRESS: ADDRESSE: Lyon & Lyon STREET: Suite 4700 CITY: Los Angeles STATE: California COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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STATE: California
COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                   APPLICANT: Iverson, Patrick L.
APPLICANT: Iverson, Patrick L.
APPLICANT: Mata, John E.
TITLE OF INVENTION: Synthteic Oligodeoxyribonucleotides
TITLE OF INVENTION: Which Mimic Telomeric Sequences for Use in the Treatment
TITLE OF INVENTION: of Cancer and Other Diseases
NUMBER OF SEQUENCES: 21
CORRESPENDENCE ADDRESS:
ADDRESSEE: Zarely, McKee, Thomte, Voorhees, & Sease
STREET: Bol Grand Suite 3200
CITY: Des Moines
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,097A
FILING DATE: 31-JAN-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                               US-08-381-097A-5/c
; Sequence 5, Application US/08381097A
; Patent No. 5643890
; GENERAL INFORMATION:
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Patent No. 5645986
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Woodring E. Wright
Elizabeth Blackburn
Nam Woo Kim
Calvin B. Harley
Scott L. Weinrich
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Michael J. McEachern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: UnmC
TELECOMUNICATION INFORMATION:
TELEPHONE: 515-288-3667
TELEFAX: 515-288-1338
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: NEbel, Heidi S
REGISTRATION NUMBER: 37,719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Michael D. West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homayoun Vaziri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Iowa
COUNTRY: United States
ZIP: 50309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: Bingle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRE ADDRESSES: Zarely STREET: 801 Grand CITY: Des Moines STREET: 802 Grand CITY: Des Moines STATE: 10wa COUNTEX: United STATE: 10wa COMPUTER EADABLE FO MEDIUM TYPE: Flop COMPUTER: 1BM PC COMPUTER: 131-0.

COMPUTER: NEADABLE FO COMPUTER: 110 MUBBE FOR EADABLE FO COMPUTER: 110 MUBBE FOR EADABLE FO COMPUTER: 110 MUBBE FOR EADABLE FOR 
               TTAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
US-08-153-051B-4/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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Sequence 3, Application US/08670999;
Patent No. S849727;
GENERAL INFORMATION:
APPLICANT: Porter, Thomas R.
TITLE OF INVENTION: Compositions and Methods for Altering TITLE OF INVENTION: the Biodistribution of Biological Agents;
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zarley, McKee, Thomte, Voorhees & Sease;
STREET: 801 Grand Suite 3200
CITY: Des Moines
STATE: Down
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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COUNTRY: United States
ZIP: 50309
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/670,999
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Nebel, Heidi S.
REGISTRATION NUMBER: 37,719
REFERENCE/OCKET NUMBER: unmc 107A
TELECOMMULICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 6; DB 2; L
100.0%; Pred. No. 6.8e+07;
                              SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/151,477A
FILING DATE: No. 5830644ember 12, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/038,766
FILING DATE: March 24, 1993
ATTORNEY,AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 202/189
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFAX: 67-3510
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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Best Local Similarity 100..
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LENGTH: 6 base pairs
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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APPLICANT: Jerry W. Shay
APPLICANT: Jerry W. Shay
APPLICANT: Woodring E. Wright
APPLICANT: Woodring E. Wright
APPLICANT: Calvin B. Harley
APPLICANT: Catherine Strah
APPLICANT: Catherine Strah
APPLICANT: Michael J. McEachern
APPLICANT: McMichael J. McEachern
APPLICANT: McMichael J. McEachern
APPLICANT: McMichael J. McMichael J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 6; DB 1; Length 6; 100.0%; Pred. No. 6.8e+07;
SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/337,684
FILING DATE: No. 5686306ember 10, 1994
CLASSIFUCATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION NUMBER: 08/15,477
FILING DATE: No. 5686306ember 12, 1993
APPLICATION NUMBER: 08/15,051
FILING DATE: No. 5686306ember 12, 1993
APPLICATION NUMBER: 08/06,952
FILING DATE: May 13, 1993
APPLICATION NUMBER: 07/882,438
FILING DATE: May 13, 1992
APPLICATION NUMBER: 07/882,438
FILING DATE: May 13, 1992
APPLICATION NUMBER: 210/085
FILING DATE: May 13, 1992
APPLICATION NUMBER: 210/085
FILING DATE: May 13, 1992
ATPORNEY AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 210/085
TELECOMMUNICATION INFORMATION:
TELEFAM: (213) 955-0440
TELECOMMUNICATION INFORMATION:
TELEFAM: (213) 955-0440
TELECOMMUNICATION NUMBER: 210/085
TELECOMMUNICATION NUMBER: 3207
TELECOMMUNICATION 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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STATE: California
COUNTRY: U.S.A.
ZIP: 30071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM COMDETIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDESULT 5

CFS-08-151-477A-4/C

Sequence 4, Application US/08151477A

Applicant Operation US/08151477A

Sequence 4, Application US/0815147A

Sequence 4, Ap
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NAME: Warburg, Richard J
REGISTRATION NUBER: 32,
REPRENCE/DOCKET NUBER: 32,
REPERENCE/DOCKET NUBER: 32,
RELEPHONE: (213) 489-160
TELECOWUNICATION INFORWATI
TELERA: 67-3510
INPORMATION FOR SEQ 1D NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 6 base pairs
LENGTH: 6 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
CONDUCCY: linear
COPOLLOGY: linear
C
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us-09-540-843-11.szlm30.rni

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Length 6;
                                         APPLICANT: Woodring E. Wright
APPLICANT: Woodring E. Wright
APPLICANT: Bilzabeth H. Blackburn
APPLICANT: Bilzabeth H. Blackburn
APPLICANT: Bilzabeth H. Blackburn
APPLICANT: Homayoun Vaziri
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
TITLE OF INVENTION: TECLOMERE LENGTH AND/OR
TITLE OF INVENTION: TECLOMERE LENGTH AND/OR
TITLE OF INVENTION: TECLOMERE AND OR
TITLE OF INVENTION: TECLOMERASE ACTIVITY
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.8e+07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: 5.25 DIBACTOR, 1.14 PLD MEDIUM TYPE: 810 CREATING SYSTEM: IBM Compatible OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: FeatSEQ for Windows 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/819,867 FILING DATE: MARCH 14, 1997 CLASSIFICATION BATA: APPLICATION NUMBER: 08/153,051 FILING DATE: NO. 6007989ember 12, 1993 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Chambers, Daniel M.
REGISTRATION NUMBER: 34,51
REFERENCE/DOCKET NUMBER: 224/232
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Elizabeth H. Blackburn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 27, Application US/08819867; Patent No. 6007989
                       J. Mceachern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Catherine M. Strahl
Michael J. Mceacheri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jerry Shay
Woodring E. Wrigh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Calvin B. Harley
Scott L. Weinrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Michael D. West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (213) 489-160
TELEXA: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 6 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 6; Conserv
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US-08-729-598-4

i Sequence 4, Application US/08729598

i Sequence 4, Application US/0872998

i Sequence 4, Application US/087298

i Sequence 4, Application US/0872
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                                                                         Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 27627
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: PROPER PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,598
FILING DATE: 11-OCT-1996
CLASSIFICATION: 530
                                                                         DB 2; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: Biswas, Sorojini J.
REGISTRATION NUMBER: 39,111
REFERENCE/DOCKET NUMBER: 5051-301A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 854-1400
TELEPHONE: (919) 854-1401
TELEPHONE: (919) 854-1401
SEQUENCE CHARACTERISTICS:
                                                                            Score 6;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 6; 100.0%; Pred. No
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Patent No. 6007989
GENERAL INFORMATION:
                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: not relevant MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Michael D. West
APPLICANT: Calvin B. Harle,
APPLICANT: Scott L. Weinri
                                               Query Match 100.
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 6 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
; ANTI-SENSE:
US-08-670-999-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-729-598-4
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us-09-540-843-11.szlm30.rni

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/desc = "peptide nucleic acid (PNB),
where (deoxy)ribose-phosphate linkages are replaced by
N-(2-aminoethyl)glycine units linked to nucleotide bases via
glycine amino nitrogen through a methylenecarbonyl linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 6; DB 3; Length 6; 100.0%; Pred. No. 6.8e+07;
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   COUNTRY: USA
ZIP: 94111-3814
COMPUTER RADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,019A
FILING DATE: 09-UW-1996
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REGISTRATION NUMBER: 32,944
REGISTRATION NUMBER: 32,944
REGISTRATION NUMBER: 32,946
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/018,545
FILING DATE: Concurrently Herewith
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PRIOR APPLICATION NUMBER: US 60/037,295
FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UTSB:654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    other nucleic acid
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Best Local Similarity 100.

Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TTAGGG 6
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DESCRIPTION:
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; Sequence No. 6015710
; GENERAL INFORMATION:
APPLICANT: Shay, Jerry W.
APPLICANT: Wight, Woodring E.
APPLICANT: Orey, David,
APPLICANT: Orey, David,
TITLE OF INVENTION: Modulation of Mammalian Telomerase by
TITLE OF INVENTION: Peptide Nucleic Acids
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 6; DB 3; Length 6; 100.0%; Pred. No. 6.8e+07; tive 0; Mismatches 0; Indels
                         Homayoun Vaziri
FENTION: THERAPY AND DIAGNOSIS OF
FENTION: CONDITIONS RELATED TO
FENTION: TECLOMERE LENGTH AND/OR
FENTION: TELOMERASE ACTIVITY
                                                                                                                                                                                                                                                                                                                      CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Diskette, 1.44 Mb
MEDIUM TYPE: 3.5 Diskette, 1.44 Mb
MEDIUM TYPE: STORAGE
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM CC. DOS 5.0
SOFTWARE: FeatSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,867
FILING DATE: March 14, 1997
CLASSIFICATION: 435
PRIOR APPLICATION BATA:
APPLICATION NUMBER: 08/153,051
FILING DATE: NO. 6007989ember 12, 1993
                                                                                                                                                                                                                 AUDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Chambers, Daniel M.
REGISTRATION NUMBER: 34.561
REFERENCE/DOCKET NUMBER: 224
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEO ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 6; Conservative
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TYPE: nucleic acid
Nam Woo Kim
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                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Ly
                                                  TITLE OF INVENTION: THE TITLE OF INVENTION: CO TITLE OF INVENTION: TE TITLE OF INVENTION: TE NUMBER OF SEQUENCES: 8
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COMPUTER: BACKE
COMPUTER: B
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US-08-630-019A-1
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Gaps
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TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
CONDITIONS RELATED TO
TECLOMERE LENGTH AND/OR
TELOMERASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: FastSEQ for Windows 2.0
                                                                                                                                                                                                                                                                                                                                      Mismatches
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APPLICATION NUMBER: US/09/378,535
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              CURRENT APPLICATION NUMBER: US/09/608,636A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/09378535
Patent No. 6551774
GENERAL INFORMATION:
APPLICANT: Michael D. West
Calvin B. Harley
Scott L. Weinrich
Catherine M. Strahl
Michael J. Mceachern
Jerry Shay
Woodring E. Wright
Elizabeth H. Blackburn
Nam Noo Kim
                       CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/142,173
PRIOR PILING DATE: 1999-07-10
PRIOR FILING DATE: 1999-07-01
PRIOR PILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: UP 11-307576
PRIOR PILING DATE: 1999-10-28
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Chambers, Daniel M. REGISTRATION NUMBER: 34,561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 20-Aug-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                        ; OTHER INFORMATION: oligonucleotide US-09-608-636A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                          LENGTH: 6
TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENČE ADDRESS:
ADDRESSEE: Lyon &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Los Angeles
STATE: California
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Best Local Similarity 100.
Matches 6; Conservative
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TITLE OF INVENTION: Telomerase Inhibitors and Methods of Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                           100.0%; Score 6; DB 3; Length 6; 100.0%; Pred. No. 6.8e+07;
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                                                                                                                                                                                                            0; Mismatches
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Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Geron Corporation
APPLICANT: Kyowa Hakko Kogyo Co., Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chin, Allison C.
Holcomb, Ryan C.
Piatyszek, Mieczyslaw A
Singh, Upinder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09608636A
Patent No. 6518268
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Yamashita, Yoshinori
Endo, Kaori
Yamaguchi, Hiroyuki
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tolman, Richard L.
Akama, Tsutomu
Kanda, Yutaka
                TELEFAK: (512) 418-301
TELEFAK: (512) 474-7577
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: PS-ODN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                         LENGTH: 6 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity
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Best Local Similarity
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APPLICANT:
                                                                                                                                                                                                            Matches
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                                 TYPE: nucleic acid

; STRANDEDNESS: single

; POPOLOGY: linear

US-09-378-535-27:
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Job time : 23.4276 secs
          LENGTH: 6 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/378,535
FILING DATE: 20-Aug-1999
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/819,867
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELOMERASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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REGISTRATION NUMBER: 34,561
REFERENCE/DOCKET NUMBER: 224/232
TELECOMMULCATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Michael D. West
Calvin B. Harley
Scott L. Weinrich
Catherine M. Strahl
Michael J. Meachern
Jerry Shay
Woodring E. Wright
Elizabeth H. Blackburn
Nam Woo Kim
                                                                                                                                                                                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-378-535-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTAGGG 6

EBULT 15

TAGGG 6

TTAGGG 7

TTAGG 7

TTAGGG 7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                 TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                      LENGTH: 6 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 27:
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                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 6; Conservative
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Sequence 1296, Ap Sequence 1297, Ap Sequence 1298, Ap Sequence 56, Appl Sequence 58, Appl Sequence 613, Ap Sequence 614, Ap Sequence 294, Appl Sequence 294, Appl Sequence 294, Appl

Sequence 63, Appl Sequence 57, Appl

Sequence 44, Sequence 57,

Sequence Sequence

Sequence Sequence

Appli

Sequence 2,

Sequence 6, Appli Sequence 4, Appli Sequence 4, Appli Sequence 58, Appl Sequence 19, Appl Sequence 41, Appl

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; OTHER INFORMATION: Description of Artificial Sequence: telomeric; CTHER INFORMATION: DNA of man US-09-817-387-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 29, Application US/09817387

Bacent No. US20010039263A1

GENERAL INFORMATION:

TITLE OF INVENTION: Chimeric Oligonucleotides and the Use Thereof FILE REFERENCE: 101195-24

CURRENT APPLICATION NUMBER: US/09/817,387

CURRENT FILING DATE: 2001-03-26

PRIOR APPLICATION NUMBER: DE 197 20 151.2

PRIOR PILING DATE: 1997-05-02

NUMBER OF SEQ ID NOS: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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US-10-122-633-12

US-09-730-893-6

US-09-940-173A-6

US-09-940-173A-4

US-10-330-627-92

US-10-330-627-92

US-10-330-627-1296

US-10-330-627-1296

US-10-330-627-1296

US-10-330-627-1296

US-10-330-627-1296

US-10-330-627-1296

US-10-330-627-1296

US-10-330-627-1296

US-10-033-145-56

US-10-033-145-1694

US-10-033-145-1694

US-09-037-351-2

US-09-92-294

US-09-92-310-4

US-09-92-310-4

US-09-942-310-4

US-09-942
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Patent No. US2001001681A1
GENERAL INFORMATION:
APPLICANT: Fillon, Mario
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ORGANISM: Artificial Sequence
            Query Match 100.
Best Local Similarity 100.
Matches 6; Conservative
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US-09-735-363A-49
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Sequence 49, Appl
                                                                                                                                                                                                December 31, 2003, 17:10:00 ; Search time 69.9494 Seconds (without alignments) 296.896 Million cell updates/sec
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Sequence 63,
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Sequence 1,
Sequence 3,
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/PCT NEW PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/USO7_NEW PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

8: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

13: /cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*

14: /cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*

15: /cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*

16: /cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*

17: /cgn2_6/ptodata/1/pubpna/USO0_NEW PUB.seq:*

18: /cgn2_6/ptodata/1/pubpna/USO0_NEW PUB.seq:*

18: /cgn2_6/ptodata/1/pubpna/USO0_NEW PUB.seq:*

18: /cgn2_6/ptodata/1/pubpna/USO0_NEW PUB.seq:*

18: /cgn2_6/ptodata/1/pubpna/USO0_NEW PUB.seq:*
                              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Animum DB seq length: 0 faximum DB seq length: 30 faximum Match 0 maximum Match 0 maximum Match 100 faximum Match 100 fax
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US-09-940-173A-1
US-10-255-535-8
US-10-336-265-1
US-10-336-265-4
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US-10-336-265-4
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US-10-232-927A-27
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US-09-735-363A-49
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Gapop 10.0 , Gapext 1.0
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                            APPLICANT: HIGHEY, LAURENCE H.

TITLE OF INVENTION: INHIBITION OF HUMAN TELOMERASE BY A
TITLE OF INVENTION: INHIBITION OF HUMAN TELOMERASE BY A
TITLE OF INVENTION: G-QUADRUPLEX-INTERACTION COMPOUND
FILE REPERENCE: UTSB: 679USD2
CURRENT APPLICATION NUMBER: US/09/940,173A
CURRENT FILING DATE: 2002-06-24
FRIOR APPLICATION NUMBER: 09/730,893
FRIOR FILING DATE: 2000-12-05
FRIOR PRICK APPLICATION NUMBER: 60/073,629
FRIOR FILING DATE: 1999-04-02
FRIOR FILING DATE: 1998-04-02
SOFFWARE: PATENTING DATE: 1998-04-02
SOFFWARE: PATENTING DATE: 2.1
SEQ ID NO 1
LENGTH.66
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100.0%; Pred. No. 5.6e+08;
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APPLICANT: Geron Corporation
APPLICANT: Gryaznov, Sergei
APPLICANT: Gryaznov, Sergei
APPLICANT: Tolman, Richard L.
APPLICANT: Tolman, Richard L.
APPLICANT: Tolman, Richard B.
TITLE OF INVENTION: Oligonucleotide Conjugates
FILE REPERENCE: 072/002P
CURRENT APPLICATION NUMBER: US/10/255,535
CURRENT FILING DATE: 2002-09-25
PRIOR FILING DATE: 2002-03-21
PRIOR FILING DATE: 2002-03-21
PRIOR FILING DATE: 2002-03-21
PRIOR APPLICATION NUMBER: US 60/278,322
PRIOR RILING DATE: 2001-03-23
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US-10-336-265-1
; Sequence 1, Application US/10336265
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Publication No. US20030138814A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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APPLICANT: Phillip, Nigel
TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
FILE REFERENCE: 02811-0181
CURRENT PPLICATION NUMBER: US/09/735,363A
CURRENT FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: 60/170,325
PRIOR PILING DATE: 1999-12-13
PRIOR PLILING DATE: 1999-12-13
PRIOR PLILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PatentIn version 3.0
SEQ ID NO 49
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APPLICANT: FEDOROPF, OLEG Y.
APPLICANT: ASLAZAK, MIGUEL
APPLICANT: HURLEY, LAURENCE H.
TITLE OF INVENTION: INHIBITION OF HUMAN TELOMERASE BY A
TITLE OF INVENTION: G-QUADRUPLEX-INTERACTION COMPOUND
FILE REPERENCE: UTSB:679USCI
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Os-0
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CURRENT FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: 09/244,675
PRIOR FILING DATE: 1999-04-02
PRIOR PLING DATE: 1999-04-02
PRIOR PLING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PACENTIN VET: 2.1
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Sequence 1, Application US/09730893

Sequence 1, Application US/09730893

Spatent No. US200201072881

CENERAL INFORMATION:
APPLICANT: KERWIN, SEAN M.
APPLICANT: SEDRORCE, OLEG Y.

APPLICANT: SALAZAR, MIGUEL

APPLICANT: HURLEY, LAURENCE H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09940173A Publication No. US20030040525A1
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
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Best Local Similarity
Matches 6; Conserv
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SEQ ID NO 1
LENGTH: 6
TYPE: DNA
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APPLICANT: Kool, Eric T.
TITLE OF INVENTION: Telonere-Encoding Synthetic DNA Nanocircles, and their use for TITLE OF INVENTION: Telonetion of Telonere Repeats
FILE REFERENCE: 12665.0021.NPUS01
CURRENT APPLICATION NUMBER: US/10/336,265
CURRENT FILING DATE: 2003-01-03
PRIOR APPLICATION NUMBER: US 60/345,056
PRIOR FILING DATE: 2002-01-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 64, Application US/10336265
Publication No. US20030148988A1
GENERAL INFORMATION:
APPLICANT: Kool, Exic T.
TITLE OF INVENTION: Telomere-Encoding Synthetic DNA Nanocircles, and their use for TITLE OF INVENTION: The Elongation of Telomere Repeats
FILE REPERENCE: 12665.0021.NPUS01
CURRENT APPLICATION NUMBER: US/10/336,265
CURRENT FILING DATE: 2002-01-03
PRIOR PRIOR PRIOR APPLICATION NUMBER: US 60/345,056
RRIOR FILING DATE: 2002-01-04
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Patentin Version 3.2
SEQ ID NO 64
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100.0%; Pred. No. 5.6e+08;
tive 0; Mismatches 0;
                                                                                        DB 13; I
5.6e+08;
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66.7%; Pred. No. 5.6e+08;
tive 2; Mismatches 0
                                                                                                                          Mismatches
                                                                                        Score 6;
Pred. No.
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Publication No. US20030148988A1
GENERAL INFORMATION:
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                                                                                        100.0%;
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SOFTWARE: Patentin version 3.2
SEQ ID NO 63
LENGTH: 6
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Best Local Similarity 66.7
Matches 4; Conservative
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; ORGANISM: Homo sapiens
US-10-336-265-64
                 TYPE: RNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Homo sapiens
                                                                                      Query Match
Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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US-10-336-265-64
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                                                     US-10-336-265-4
     LENGTH: 6
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TITLE OF INVENTION: The Blongation of Telomere Repeats
TITLE OF INVENTION: the Blongation of Telomere Repeats
TITLE OF INVENTION: the Blongation of Telomere Repeats
FILE REPERENCE: 1265.0021.NPUS01
CURRENT APPLICATION NUMBER: US/10/336,265
CURRENT FILING DATE: 2003-01-03
PRIOR PILING DATE: 2003-01-04
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Patentin version 3.2
SEQ ID NO 1
LENGTH: 6
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Publication No. US200301489881
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Telomere-Encoding Synthetic DNA Nanocircles, and their use for TITLE OF INVENTION: the Elongation of Telomere Repeats
FILLE REFERENCE: 12665.0021.NPUS01
CURRENT APPLICATION NUMBER: US/10/336,265
CURRENT FILING DATE: 2003-01-03
PRIOR APPLICATION NUMBER: US 60/345,056
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn version 3.2
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Publication No. US20030148988A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 6; Conserv
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TTAGGG 1
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US-10-336-265-4/C
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ORGANISM: Hom
Section 136-265-3
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100.0%; Score 6; DB 13; Length 6;
Best Local Similarity 100.0%; Pred. No. 5.6e+08;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                       Homayoun Vaziri
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
CONDITIONS RELATED TO
TEOLOMERE LENGTH AND/OR
TELOMERASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/232,927A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 29-Aug-2002
CLIASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/378,535
FILING DATE: 20-Aug-1999
APPLICATION NUMBER: 08/819,867
FILING DATE: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Chambers, Daniel M.
REGISTRATION NUMBER: 34,561
REFERENCE/DOCKET NUMBER: 224/232
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: single ropology: linear sequence DESCRIPTION: SEQ ID NO: 27: US-10-232-927A-27
                                                                                               Michael J. Mceachern
Jerry Shay
Woodring E. Wright
Elizabeth H. Blackburn
Nam Woo Kim
                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS: Lyon
ADDRESSEE: Lyon
STREET: 633 West Fifth Street
            GENERAL INFORMATION:
APPLICANT: Michael D. West
Calvin B. Harley
Scott L. Weinrich
Catherine M. Strahl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 27
Publication No. US20030190638A1
                                                                                                                                                                                                                                                                                                                                                   Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 90071-2066
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                              CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                             Homayoun Vaziri
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
                                                                                                                                                                                                                                                                                             CONDITIONS RELATED TO TEOLOMERE LENGTH AND/OR TELOMERASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFFWARE: FRSEUSED for Windows 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/10/232,927A
FILING DATE: 29-Aug-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/378,535
FILING DATE: 20-Aug-1999
APPLICATION NUMBER: 08/819,867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Chambers, Daniel M.
REGISTRATION NUMBER: 34,561
REFERENCE/DOCKET NUMBER: 224/232
TELECOMMUNICATION INFORMATION:
                                                                                           APPLICANT: Michael D. West
Calvin B. Harley
Scott L. Weinrich
Catherine M. Strahl
Michael J. Mceachern
Jerry Shay
Woodring E. Wright
Elizabeth H. Blackburn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 6 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                Sequence 9, Application US/10232927A
Publication No. US20030190638A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            storage
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INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 80
                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                             Nam Woo Kim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
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Best Local Similarity
                                                                                    GENERAL INFORMATION
                                  US-10-232-927A-9
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Sequence II, Application US/10122630
Publication No. US20030032610A1
GENERAL INFORMATION:
APPLICANT: Gilchreet, Barbara A.
APPLICANT: Eller, Mark S.

; Sequence 27, Application US/10232927A

RESULT 12 US-10-232-927A-27/c

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Sequence 11, Application US/10122633
; Publication No. US20030032611A1
; Publication No. US20030032611A1
; GENERAL INFORMATION:
    APPLICANT: Glichreet, Barbara A.
; APPLICANT: Blex, Mark S.
; APPLICANT: Blex, Mark S.
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using; TITLE OF INVENTION: Oligonucleotides
; FILE REFERENCE: 0054.1088-019
; CURRENT APPLICATION NUMBER: US/10/122,633
; CURRENT FILING DATE: 2000-03-31
; PRIOR PILIOR DATE: 2000-03-31
; PRIOR PILIOR DATE: 2001-03-30
; SOFTWARE: PRECED FOR Windows Version 4.0
; SEQ ID NO 11
ELENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Synthetic DNA Fragment
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6 TTAGGG 1
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100.0%; Score 6; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 5.6e+08;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 6; DB 15; Length 6; Similarity 100.0%; Pred. No. 5.6e+08; 6; Conservative 0; Mismatches 0; Indels
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Publication No. US20030032610A1
GENERAL INFORMATION:
APPLICANT: Glichzeet, Barbara A.
APPLICANT: Eller, Mark S.
APPLICANT: Yaar, Mina
TITLE OF INVENTION: Method to Inhibit Cell Growth Using
TITLE OF INVENTION: Oligonucleotides
FILE REPRESENCE: 0054.1088-018
CURRENT APPLICATION NUMBER: US/10/122,630
CURRENT PILING DATE: 2002-04-12
                                       INVENTION: Method to Inhibit Cell Growth Using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONTRIBER OF SEQ ID NOS: 15

SOFTWARE: FastSEQ for Windows Version 4.0

TYPE: DNA

ORGANISM: Artificial Sequence
FRATURE:
O
                      TITLE OF INVENTION: Method to Inhibit Cell Girlt Corner of Invention: Oligonucleotides FILE REPERENCE: 0054.1088-018
CURRENT APPLICATION NUMBER: US/10/122,630
CURRENT FILING DATE: 2002-04-12
PRIOR PAPLICATION NUMBER: US 08/467,012
PRIOR FILING DATE: 1995-06-06
PRIOR FILING DATE: 1996-06-03
PRIOR APPLICATION NUMBER: US 09/048,927
PRIOR APPLICATION NUMBER: US 09/048,927
PRIOR APPLICATION NUMBER: US 09/540,843
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
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PRIOR FILING DATE: 1995-06-06
PRIOR FILING DATE: 1995-06-03
PRIOR FILING DATE: 1996-06-03
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR PRILING DATE: 2000-03-31
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PastSEQ for Windows Version 4.0
SSETURN 12
LENGTH: 6
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US-10-122-630-12
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ORGANISM: Artificial Sequence
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               Length 6;
                                         0; Indels
              Score 6; DB 15; I
Pred. No. 5.6e+08;
100.0%; Scortion 100.0%; Pred. No. Str. 0; Mismatches
                                                                                                                                      Search completed: January 1, 2004, 01:10:39 Job time : 69.9494 secs
            Query Match
Best Local Similarity 100.
Matches 6; Conservative
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Gaps

Homo sapiene

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

AW248826

ACCESSION

DEFINITION

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AW248836 21 bp mRNA linear EST 07-JAN-2000 2821108.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821108 3',
                                                                                                                          polyadenylated.
Plate: LLCWS row: N column: 1
High quality sequence stop: 21.
Location/Qualifiers
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AW248836
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AW248836/c
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Gaps ö

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Other ESTS: 2821108.5prime

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.inin.gov

Tissue Procurement: DCTD/DTP CDNA Library Preparation: Ling
Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.

Consortium (LIMI) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LiML at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PRRED From University of Washingtion Genome Center
Trimming: cross match from University of Washingtion Genome Center
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washingtion Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 10
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: Trace file contained 21 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a Xhoi site followed by a run of 14 or more T residues
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                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 21)

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National Institutes of Health, Mammalian Gene Collection (MGC)
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High quality sequence stop: 10.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:2821108"
                                                                 Homo sapiens (human)
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5, Conserva
                                                                                                         Homo sapiens
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AUTHORS
TITLE
JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Straubberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboractory CDNA Library Arrayed by: The I.M.A.G.E.
Gonsortium (LLNL) DNA Sequencing by: Barkeley MGC sequencing
project Clone distribution: MGC Clone distribution information can
be found through the I.M.A.G.E. Consortium/LLML at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PRRED from University of Washingtion Genome Center. Vector
Trimming: cross match from University of Washingtion Genome Center.
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washingtion Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 21
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: Trace file contained 21 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a Xhoi site followed by a run of 14 or more T residues
at the beginning of the sequence, this CDNA insert was
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//db_xref="taxon:9606"
/clone="INAGE:2821066"
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/clone="INAGE:2821066"
/clone="HAGC3"
/lab_host="DHIOB (phage-resistant)"
/clone="Organ: lung; Vector: pOTB7; Site 1: Xho1; Site 2:
RcoR1; cDNA made by oligo-dT priming. Directionally
cloned into EcoR1/Xho1 sites using the following 5:
adaptor: GGCACGGG(G). Size-selected by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
4 a 3 c 11 t.
AW248826 21 bp mRNA linear EST 07-JAN-2000
2821056.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821056 3',
mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
Other ESTs: '2821056.5prime
                                                                                                                                                                       AW248826.1 GI:6591819
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TA199G02Q 20 bp DNA linear GSS 13-DEC-2000
T. brucei sheared genomic DNA clone 199g02, reverse sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Constructed at the Institute for Genomic Research (TICR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma bruce; (TREU927/4 GUTAL 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
innert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              project, Sanger Centre, The Wellcome Trust Genome sequencing Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
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Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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100.0%; Pred. No. 6.6e+05;
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'organism="Trypanosoma brucei"
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100.0%; Pred. No. ...
0; Mismatches
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    .20
    /organism="Trypanosoma"
/mol_type="genomic DNA"
/strain="TREU927"

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                                                                                                         /db_xref="taxon:5691"
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AL476798.1 GI:11843362
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TA199G02Q/c
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AW248826/c
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JOURNAL
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                                                                                                                                                                                                                                                    (http://www.iax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated inducible derivative of plasmid R1. The vector was ligated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored weetor DNA, and transformed into chemically-competent B. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSS 13-DEC-2000
                                                                                                                                             /lab host="E. coli strain XL10-Gold, T1-resistant, F-"/clone_lib="Mouse 10kb plasmid UUGC2M library"/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (female) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Rockville, MD. Genomic DNA isolated from a cloned population of
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TA158A03P 20 bp DNA linear GSS 13-DE
T. brucei sheared genomic DNA clone 158a03, forward seguence,
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Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 6; DB 28; Length 20; 100.0%; Pred. No. 6.6e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                         Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                         /mol_type="genomic DNA'
/strain="C57BL/6J"
                                                                                  /db_xref="taxon:10090"
/clone="UUGC2M0227G21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genomic survey sequence.
AL472050
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L (bases 1 to 20)
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                                                                                                                                                                                                                         /lab hose="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42ry; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources /documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifica at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarces gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4712114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for amplcillin resistance."
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weisse, R.,
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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100.0%; Pred. No. 6.6e+05;
ive 0; Mismatches 0;
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Insert Length: 10000 Std Error: 0.00
Plate: 0071 row: D column: 09
Seg primer: CACACAGGAAACAGCTATGACC
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University of Utah Genome Center
University of Utah
mol_type="genomic DNA"
                                                                                               db_xref="taxon:10090"
clone="UUGC1M0542G17"
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Location/Qualifiers
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                                                                                                                                                                                                         /sex="Male
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Fax: 801 585 7177
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/clone lib="Mouse lobb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G78BL/60 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide Kinase. Adaptor oilgonicleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gal
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
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adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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2M0227G21R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0227G21 R, genomic survey sequence.
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2 (bases 2 to 20)

2 (bases 2 to 20)

3 (bases 2 to 20)

3 (bases 2 to 20)

4 (bases 2 to 20)

4 (bases 2 to 20)

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7 (bases 2 to 20)

8 (bases 2 to 20)

8 (bases 2 to 20)

9 (bases 2 to 20)
                                                                                                                                                                   /sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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Insert Length: 10000 Std Error: 0.00
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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Location/Qualifiers
                                                                                                                        /clone="UUGC2M0071D09"
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Fax: 801 585 7177
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us-09-540-843-11.szlm30.rst

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Plate: 0542 row: G column: 17
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
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University of Utah Genome Center
University of Utah
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clone="UUGC1M0467010"
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Matches 6; Conserv
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                                                                                                                                                                                                                        (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwalp4 (gqi 4732114[gb]AR129772.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xillo-Gold (Stratagene) cells and selected for ampicillin resistance."
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University of Utah Genome Center
University of Utah
Wm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                           /lab host="E. Coli strain XLIO-Gold, T1-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
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Fax: 801 585 7177
Email: ddunn@qenetics.utah.edu
Insert Length: 10000 Std Error: 0.(
Plate: 0467 row: 0 column: 10
Seq primer: CACACAGGAAACACCTATGACC
Class: plasmid ends
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Mus musculus
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Matches 6; Conservative
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMAP2 (gil 4/732114 [gb] AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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20 bp DNA linear GSS 14-DEC-200
1M0542G17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0542G17 F, genomic survey sequence.
                                /clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
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100.0%; Pred. No. 6.6e+05;
iive 0; Mismatches 0;
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Fax: 801 585 7177
Email: dduun@genetics.utah.edu
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us-09-540-843-11.szlm30.rst

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AZ345513 20-SEP-2000 1M0080J04F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0080J04 F, genomic survey sequence.
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84112, USA
                                                                                         /mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line
                                                                                                                                                                                                                                            SP6-SalI-CCACGCGTCCG-5prime.cDNA-polyA-CC-Not1-T7; Note: Sequencing granted in the context of the GABI-Beet project, local Pir Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (Dases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished
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Seg primer: SP6; CATACGATTTAGGTGACACTATAG.
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100.0%; Pred. No. 6.6e+05;
Live 0; Mismatches 0;
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/organism="Beta vulgaris"
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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University of Utah Genome Center
University of Utah
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High quality sequence stop: 20.
Location/Qualifiers
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                             /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/mouse="Vector: PWD42Dr; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dhares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated by sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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S015529-024-026-P04-SP6 MPIZ-ADIS-024-developing root Beta vulgaris
CDNA clone 024-026-P04 5-PRIME, mRNA sequence.
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    (bases 1 to 20)

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Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
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Emall: welssha@mpiz-koeln.mpg.de
Insert Length: 20 Std Error: 0.00
Plate: 26 row: P column: 04
                     Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
                                                                                                                                    organism="Mus musculus"
                                                                                                                                                              'mol_type="genomic DNA"
'strain="C57BL/6J"
                                                                                                                                                                                                      'db_xref="taxon:10090"
'clone="UUGC2M0102N07"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Win's Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
,M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A.,
mouse whole genome scaffolding with paired end reads from 10kb
plasmid niests
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Insert Length: 10000 Std Error: 0.00
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Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|q13214]qb]hg129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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2M0102N07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0102N07 R, genomic survey sequence.
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/clone lib="Mouse 10kb plasmid UDGCIM library."
/note="WetCr: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                    organism="Mus musculus"
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University of Utah Genome Center
University of Utah
                                                                                                                                                                                                         /mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0443A17"
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
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                                                                                                                                                                                                                                                                                                                          /lab host="E. Coli strain XLIO-Gold, T1-resistant, F-"/clone_lib="Mouse 10kb plasmid UUGCIM library"/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C37BL/6J (male) was obtained from the Jackson
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                                                                                                                           /organism="Mus musculus"
/mol_type="genomic DNA"
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Class: plasmid ends
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Plate: 0200 row: F column: 10
Seg primer: CACACAGGAAACAGCTATGACC
                 High quality sequence stop: 19.
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6; Conservative
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washingtion Genome Center: http://www.genome.washington.edu Low Quality Sequence: 15 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 16 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this CDNA insert was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSS 03-OCT-2000
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10. Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cone libe Will MGC 7"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
BCORI; CDNA made by oligo-dT priming. Directionally
cloned into BCORI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:2819454"
/tissue type="small cell carcinoma"
/cell line="MGC3"
/lab_nost="DH10B (phage-resistant)"
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Fax: 801 585 7177
Email: ddunnagenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0154 row: G column: 12
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Plate: LLCM1 row: K column: 7
High quality sequence stop: 15.
Location/Qualifiers
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be considered by the constant of 
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalp42 (gil 4732114 [gb] AF125072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xii0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(bases 1 to 19)

Unn,D., Adyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Menen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

Mand Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts
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1M0200F10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0200F10 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                   /lab_host="B. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UGGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/6J (male) was obtained from the Jackson
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Fax: 801 585 7177
Faxial: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory Mouse DNA Resource
                                             1. .19
/organism="Mus musculus"
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University of Utah Genome Center
University of Utah
                                                                                                         /mol_type="genomic DNA"
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/db_xref="taxon:10090"
/clone="UUGC1M0154G12"
Location/Qualifiers
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	GenCore version	Copyright (c) 1993 - 2003 Compugen Ltd.		OM nucleic - nucleic search, using sw model		Run on: December 31, 2003, 13:58:09; Search time 689:392 Seconds	21.530 Million cell updates/sec	Title: US-09-540-843-11		555 54 1	Scoring table: IDENTITY NUC		Sparched. 22781132 core 12152313056 voriding		(Trotal number of hits satisfying chosen parameters: 33330	d	Minimum DB seq Length: 0	or Tendrus on Tendrus or	Post-processing: Minimum Match 0%	Match	Listing first 45 summaries		E	c	S 2: em estrum:	 	iè		ά	 	10:1	11	12	13	4 4	9	17:	18:	19:	20:	Z ZI: em ges uni: *  N 22: em ges man: *	23.	24: em gas pro:*	25: em_gss_rod:*	26: em_gss_phg:*	28: oh gsg1:*	29: gb_ges2:*	-

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		454.3	154G12	200F10	443A17
	Description	AW248958 2819454.3	AZ392246 1M0154G12	AZ422271 1M0200F10	AZ614760 1M0443A17
SUMMARIES	ID	100.0 16 9 AW248958	AZ392246	AZ422271	AZ614760
	DB		28	28	28
•	Query Match Length DB ID	16		19	19
de	Query Match	100.0	100.0	100.0	100.0
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19         28         AZ826736         BQ593485         SN0102N07           20         28         AZ345513         AZ627174         AZ627174         AZ627174         AZ627174         AZ627174         AZ627174         AZ662909         AZ627174         AZ662909         AZ66201         AZ66210         AZ66201         AZ66210         AZ66220         AZ66220 <th>AM248958  AW248958  AW248958  16 bp mRNA linear EST 07-JAN-2000  AW248958  AW248958  AW248958  AW248958  AW248958  AW248958  AW248958  Graniata Craniata; Vertebrata; Euteleostom; Fultono sapiens  Homo sapiens  Homo sapiens  Homo sapiens  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  Momealia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  Morional Institutes of Health, Mammalian Gene Collection (MGC)  Unpublished  Contact: Robert Strausbery; Ph.D.  Email: cgapbs-r@mail.nih.gov  Tissue Procurement: DCTD/DTP CDNA Library Preparation: Ling  Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.  Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E.  Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E.  Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E.  Scores: PHRED from University of Washingtion Genome Center.  Trimming: cross_match from University of Washingtion Genome Center.</th>	AM248958  AW248958  AW248958  16 bp mRNA linear EST 07-JAN-2000  AW248958  AW248958  AW248958  AW248958  AW248958  AW248958  AW248958  Graniata Craniata; Vertebrata; Euteleostom; Fultono sapiens  Homo sapiens  Homo sapiens  Homo sapiens  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  Momealia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  Morional Institutes of Health, Mammalian Gene Collection (MGC)  Unpublished  Contact: Robert Strausbery; Ph.D.  Email: cgapbs-r@mail.nih.gov  Tissue Procurement: DCTD/DTP CDNA Library Preparation: Ling  Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.  Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E.  Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E.  Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E.  Scores: PHRED from University of Washingtion Genome Center.  Trimming: cross_match from University of Washingtion Genome Center.
	AW248958  RNA 4848958  AW248958.1  EST. HOMO SADIEN  CONTACT: RO  HOMO SADIEN  HOMO SADIEN  CONTACT: RO  HOMO SADIEN  HOMO SADIEN  SCORES: PHR  Trimming: C
	AW248958 AW248954 AW248958 AW24895
<i>Ა Ა Ა Ა Ა Ა Ა Ა Ა Ა Ა Ა Ა Ა          </i>	AW2, AW2, AW2, AW2, AW2, AW2, AW2, AW2,
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 AW248958 LOCUS DEFINITION ACCESSION EREADON KEYWORDS SOURCE ORGANISM THTLE JOURNAL COMMENT

Matches

X S

RESULT 14

g

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This sequence is a novel peptide nucleic acid (PNA), which acts as an inhibitor of mammalian, preferably human, telomerase. The PNAs hybridise specifically to an RNA component of mammalian telomerase, and include the sequence GGG for specific hybridisation to the template region of this component. PNAs can be used as probes to detect the RNA component of mammalian telomerase and as inhibitors of telomerase activity, especially in the treatment of cancer.
                                                                                                                                                                                                                                            /*tag= a
/note= "Sugar-phosphate backbone has been replaced by
                                                                                                            Peptide nucleic acid; PNA; cancer; telomerase; probe; hybridisation;
inhibitor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New peptide nucleic acids hybridising to mammalian telomerase RNA used to inhibit telomerase, for treating tumours and other proliferative diseases, also for diagnosis
                                                                        Peptide nucleic acid 15, targeted to mammalian telomerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 6; DB 18; Length 9; 100.0%; Pred. No. 2.9e+08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shay JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9 BP; 2 A; 0 C; 4 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                               a peptide backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: December 31, 2003, 15:08:16 Job time : 173.392 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Piatyszek MA,
                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 9; Page 59; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                               97WO-US05931.
                                                                                                                                                                                                                                                                                                                                                                                                                                     96US-0630019
                                     (first entry)
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Best Local Similarity 100.0
Them 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corey D, Norton JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-512647/47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GERO-) GERON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TTAGGG 6
                                                                                                                                                                                                        Key
modified_base
                                                                                                                                                                                                                                                                                                                                                                                               39-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                     39-APR-1996;
                                                                                                                                                                                                                                                                                                                        WO9738013-A1
                                     12-MAY-1998
                                                                                                                                                                                                                                                                                                                                                            16-OCT-1997.
                                                                                                                                                                   Synthetic.
AAT89240;
à
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                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                 Telomerase; proliferation; telomere; hybrid; immortalised cell; anaemia; transplantation; cell therapy; treatment; AIDS; leukaemia; lymphoma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonucleotides AATO5734-7 are examples of telomerase substrates used to increase the proliferative capacity of normal cells that express telomerase activity. The oligonucleotides allow an increase in length of telomeres in normal cells and in hybrids of normal and immortalised cells. The increase in telomere length extends the capacity of cells to replicate, esp. those treated ex vivo and used for transplantation techniques e.g. cell therapy, for the treatment of AIDS, anaemia, leukaemia or lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Increasing telomere length in cells - to increase proliferative capacity and therefore delay cellular senescence, useful in cell therapy and transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                       Length 8;
                                                                                          0; Indels
                                                     100.0%; Score 6; DB 23; I 100.0%; Pred. No. 3.2e+08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9 BP; 2 A; 0 C; 3 G; 4 T; 0 other;
                 Sequence 8 BP; 1 A; 0 C; 3 G; 2 T; 2 other;
                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                             Telomerase oligonucleotide substrate #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 12; Page 29; 38pp; English.
                                                                                                                                                                                                                                                             AAT05735 standard; DNA; 9 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shay J, West MD, Wright WE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94WO-US13130.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                                                                        01-FEB-1996 (first entry)
                                                                      Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-224051/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GERO-) GERON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                             1 TTAGGG 6
                                                                                                                                                             2 TTAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-NOV-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                   AAT05735;
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                                                     Query Match
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acopied arom augo expagator aus a longato aus esseux

WE;

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Gaps

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AAT89240 standard; DNA; 9 BP.

RESULT 15 AAT89240 ID AAT8 XX

셤

TTAGGG

Matches

us-09-540-843-11.szlm30.rng

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Sequence 8 BP; 1 A; 0 C; 4 G; 3 T; 0 other;
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The present invention relates to peptide nucleic acids (PNAs), comprising a sequence of 6-25 nucleobases, that inhibit telomerase activity in mammalian calls by hybridising to the RNA component of mammalian telomerase. The PNAs are useful as probes to detect the RNA component of mammalian telomerase and as inhibitors of telomerase activity, or to detect and/or quantitate polynucleotide having the human telomerase tNA component (hTR) sequence, as well as in forensic identification of individuals, such as paternity testing or identification of criminal suspects or unknown descendants based on the hTR gene RFLP pattern. The PNA can be further used for treating or preventing cancer, inflammation, lymphopycoliferative diseases, autoimmune disease, or neurodegenerative diseases. The PNAs in combination with other pharmaceuticals (such as antineoplastic or cytostatic agents) can be used for treating neoplasia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hyperplasia, human immunodeficiency virus (HIV) infections, acquired immunodeficiency syndrome (AIDS) and associated pathologies, and other diseases characterised by abnormal telomere metabolism or telomerase activity. The present sequence represents one of the PNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New peptide nucleic acids that hybridises to the RNA component of mammalian telomerase, useful for treating or preventing cancer, inflammation, lymphoproliferative diseases, autoimmune disease, or neurodegenerative diseases
inflammation; lymphoproliferative disease; autoimmune disease; neurodegenerative disease; neoplasia; hyperplasia; HIV; AIDS; human immunodeficiency virus; acquired immunodeficiency syndrome; telomere metabolism; mutant; cytostatic; anti-inflammatory; immunosuppressive; polyamide backbone; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
"This sequence is a peptide nucleic acid, i
contains a polyamide backbone instead of a
deoxyribose backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corey DR, Norton JC;
                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Piatyszek MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 7; Column 73; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0349532.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96US-0630019.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                        modified base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US6294650-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-JUL-1999;
                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-APR-1996;
                                                                                                                                                                                                                                                                                           Synthetic.
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a "This sequence is a peptide nucleic acid, i.e. it contains a polyamide backbone instead of a

Location/Qualifiers

1..8 /\*tag= /note=

modified\_base

Homo sapiens. Synthetic.

deoxyribose backbone"

nucleobases

or

peptide nucleic acid from U, T, A, G, C or

/note= "N= 1-50 selected

/\*tag= b

modified base

nucleic acid n T, A, G, C or

peptide from U,

"N= 1-50 g selected f

/note=

modified\_base

99US-0349532. 97US-0838545 96US-0630019

08-JUL-1999; 09-APR-1997; 09-APR-1996;

25-SEP-2001.

Mammalian; peptide nucleic acid; probe; forensic; paternity testing; human telomerase RNA component; hTR gene RFLP pattern; cancer; inflammation; lymphoproliferative disease; autcimmune disease; neurodegenerative disease; neoplasia; hyperplasia; HIV; AIDS; human immunodeficiency virus; acquired immunodeficiency syndrome; telomere metabolism; mutant; cytostatic; anti-inflammatory; immunosuppressive; polyamide backbone; ss.

PNA 34 inhibiting human and mammalian telomerase activity.

(first entry)

14-FEB-2002

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comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   telomerase. The PNAs are useful as probes to detect the RNA component of mammalian telomerase and as inhibitors of telomerase activity, or to detect and/or quantiate polymucleotide having the human telomerase RNA component (hTR) sequence, as well as in forensic identification of individuals, such as paternity testing or identification of criminal suspects or unknown descendants based on the hTR gene RFLP pattern. The PNA can be further used for treating or preventing cancer, inflammation, lymphoproliferative diseases, autoimmune disease, or neurodegenerative diseases. The PNAs in combination with other pharmaceuticals (such as antineoplastic or cytostatic agents) can be used for treating neoplasia, hyperplasia, human immunodeficiency virus (HIV) infections, acquired immunodeficiency syndrome (ALDS) and associated pathologies, and other diseases characterised by abnormal telomere metabolism or telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 given in the SEQ ID listing but is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 activity. The present sequence represents one of the PNA sequences of the invention.

Once: The present sequence is given in the SEQ ID listing but is no mentioned elsewhere in the patent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         component of
ing cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to peptide nucleic acids (PNAs), coa sequence of 6-25 nucleobases, that inhibit telomerase activity mammalian cells by hybridising to the RNA component of mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New peptide nucleic acids that hybridises to the RNA component omammalian telomerase, useful for treating or preventing cancer, inflammation, lymphoproliferative diseases, autoimmune disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Column 59; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neurodegenerative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-638024/73.
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Gaps

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Length 8; Indels

100.0%; Score 6; DB 23; I 100.0%; Pred. No. 3.2e+08; ive 0; Mismatches 0;

6; Conservative

Matches

9

ò g

Query Match Best Local Similarity

AAS15474 standard; DNA; 8 BP

RESULT 13 AAS15474

AAS15474;

Wright WE, Piatyszek MA, Corey DR, Norton JC;

(TEXA ) UNIV TEXAS SYSTEM.

Shay JW,

97US-0838545.

09-APR-1997;

04-APR-2000.

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The present sequence represents a peptide nucleic acid molecule which hybridises to the mRNA component of mammalian telomerase, and inhibits telomerase activity. Telomerase is a ribonucleoprotein enzyme that synthesizes one strand of the telomeric DNA, using as a template an 11 nucleotide sequence contained within the RNA component of the enzyme. The invention relates to DNA molecules having a sequence of no more than 25 bases, which include the sequence GTTAGG. The uncharged nature of the PNA bases, which include the sequence GTTAGG. The uncharged nature of the PNA component increases the melting temperature of associating strands, increases the rate of association with targeted nucleic acids, and affords greater resistance of degradation by proteases or nucleases. The increases the used for treating disease conditions such as cancers, neoplasia, hyperplasia, neurodegenerative diseases. Aping, human immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency syndrome) and associated pathologies, fungal infections, and other diseases characterized by abnormal telomers metabolism of the compense of extracterized by abnormal telomers metabolism of the compense of crivity, in combination with antineoplastic and other cytotoxic or cytostatic agents, antifungal agents, and other nucleotides. PNAs may be used for molecular diagnostics, labelled PNAs are used as hybridization probes to detect or quantitate polynucleotides having a human telomerase activity. The method of the present invention of individuals, e.g. paternity testing, based on hTR gene restriction fragment length polymorphism (RPLP) pattern. PNAs are also used as probes to detect the RNA component of a mammalian telomerase and as inhibitors of telomerase activity. The method of the present invention call or tened of the present invention call be used to detected an immortal or methods of the present invention call be used to detect an immortal or methods of the present invention and be used do detected an immortal or methods of the present and
activity in mammalian cells is useful as probes to detect the RNA
                                                                   component of a mammalian telomerase
                                                                                                                                                                                     Claim 6; Column 71; 45pp; English.
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Sequence 8 BP; 1 A; 0 C; 4 G; 3 T; 0 other;
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Gaps ö 100.0%; Score 6; DB 21; Length 8; 100.0%; Pred. No. 3.2e+08; 0; Indels 0; Mismatches 6; Conservative

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AAA37572 standard; DNA; 8 BP

15-AUG-2000 (first entry)

PNA sequence #30 used to inhibit telomerase activity.

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Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer; inhibitor; neoplasia; neurodegenerative disease; āging; hyperplasia; AIDS; HIV; fungal infection; forensic identification; detect; tumour; paternity testing; ss.

N-(2-aminoethyl)glycine units are linked to nucleotide bases via glycine amino N through methylenecarbonyl linker" a "Peptide nucleic acid molecule, where Location/Qualifiers

Mammalian, peptide nucleic acid, probe, forensic, paternity testing, human telomerase RNA component; hTR gene RFLP pattern; cancer;

```
The present sequence represents a peptide nucleic acid molecule which hybridises to the mRNA component of mammalian telomerase, and inhibits telomerases activity. Telomerases is a ribbonucleoprotein enzyme that synthesizes one strand of the telomeric DNA, using as a template an 11 nucleotide sequence contained within the RNA component of the enzyme. The nucleotide sequence contained within the RNA component of the enzyme. The nucleotide sequence contained within the RNA component of the enzyme. The nucleotide sequence contained within the RNA component of the enzyme. The component include the sequence GTTAGG The uncharged nature of the PNA backbone increases the melting temperature of associating strands, concers, neoplasia, hyperplasia, rectaing disease conditions such as the sequence of degradation by proteases or nucleases. The therapeutic PNAs may be used for treating disease conditions such as cancers, neoplasia, hyperplasia, neurodegenerative diseases. The therapeutic PNAs may be used for treating disease conditions and associated pathologies, fungal infections, and other immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency virus (HIV)) infection/AIDS (acquired immunodeficiency virus (HIV)) infection (AIDS (AIDS (HIV)) infection (AIDS (AI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                New peptide nucleic acid (PNA) compounds that inhibit telomerase activity in mammalian cells is useful as probes to detect the RNA component of a mammalian telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                     Corey DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neoplastic cell or tumour tissue or cancer of any origin, cell expresses telomerase activity and its RNA component.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 6; DB 21; Length 8; 100.0%; Pred. No. 3.2e+08;
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                                                                                                                                                                                                                     Norton JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8 BP; 3 A; 4 C; 0 G; 1 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                       Shay JW,
                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; Column 33; 45pp; English
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                                                                                                                     96US-0630019
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                                                                                                                                                                      (TEXA ) UNIV TEXAS SYSTEM
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                                                                                                                                                                                                                                                                    WPI; 2000-292432/25.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 TTAGGG 2
                                                                                                                       09-APR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
AAS15436
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Ecker DJ;

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This sequence is a novel peptide nucleic acid (PNA), which acts as an inhibitor of mammalian, preferably human, telomerase. The PNAs hybridise specifically to an RNA component of mammalian telomerase, and include the sequence GGG for specific hybridisation to the template region of this component. PNAs can be used as probes to detect the RNA component of mammalian telomerase and as inhibitors of telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Peptide nucleic acid molecule, where N-(2-aminoethyl)glycine units are linked to nuclectide bases via glycine amino N through a methylenecarbonyl linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia; AIDS; HIV; fungal infection; forensic identification; detect; tumour;
                                                                                                                                                                           New peptide nucleic acids hybridising to mammalian telomerase RNA used to inhibit telomerase, for treating tumours and other proliferative diseases, also for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New peptide nucleic acid (PNA) compounds that inhibit telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 8;
                                                                                         Wright WE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PNA sequence #15 used to inhibit telomerase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 6; DB 18; L
100.0%; Pred. No. 3.2e+08;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                activity, especially in the treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Norton JC,
                                                                                         Shay JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8 BP; 1 A; 0 C; 4 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wright WE, Piatyszek MA, Shay JW,
                                                                                         Piatyszek MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                Claim 9; Page 59; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0838545.
  96US-0630019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA37558 standard; DNA; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 paternity testing; ss
                                                                                         Norton JC,
                                                                                                                                WPI; 1997-512647/47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-292432/25.
                                             GERON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TTAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTAGGG
  09-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US6046307-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA37558;
                                                                                      Corey D,
                                             (GERO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
# X 4 X I X 8 X F F F X 8 X D D D D D D X 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New peptide nucleic acid (PNA) oligomers are provided which (a) consist of naturally occurring nucleobases covalently bound to a polyamide backbone and (b) hybridise to the translation initiation MGG region, 5 untranslated region (3' UTR), 3' untranslated region (3' UTR), 5 untranslated region (3' UTR), 5 untranslated region (3' UTR), 5 police junctions or coding sequence of a human immunodeficiency virus gene chosen from env, gag, pol, rev and tat.

The PNAs can be used to target RNA and single stranded DNA (spDNA) to produce antisense-type gene regulation moieties. They have utility as gene-targetted drugs for modulating HIV processes. Hence they can be used to treat AIDS and other viral infections. They are also useful in diagnostic applications and as research tools.

They are also able to form triple helices in which a first PNA strand binds with the resulting double helix or with the first PNA strand. The PNAs possess no coluble helix or with the first PNA strand. The PNAs possess no coluble helix or with the first PNA strand. The PNAs possess cellular moters.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         uptake. Further, since they contain amides of non-biological amino acids, they are biostable and resistant to enzymatic degradation by proteases. The present sequence is a specifically claimed PNA sequence (represented by the sequence of nucleobases) targetting HIV genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
"Sugar-phosphate backbone has been replaced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide nucleic acid; PNA; cancer; telomerase; probe; hybridisation;
                                                                                                                                                Oligomer hybridisable to HIV sequence and contg. peptide nucleic acid sub:unit - binds in complementary manner to DNA and RNA, and useful for modulating HIV viral activity, e.g. in treating AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 8;
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100.0%; Score 6; DB 16; I
Best Local Similarity 100.0%; Pred. No. 3.2e+08;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8 BP; 1 A; 0 C; 3 G; 4 T; 0 other;
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                                                                                                                                                                                                                                           Claim 2; Page 176; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT89239 standard; DNA; 8 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97WO-US05931
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/note=
                    (ISIS-) ISIS PHARM INC
                                                                                                      WPI; 1995-082179/11
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modified_base
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DR;

Synthetic.

AAT89239;

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Gaps

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The DNA is a variant of the telomere of the pAtT4 plasmid (ATCC 67577). (Updated on 25-MAR-2003 to correct PA field.)
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                                                                                                                                                                                                                                                               New recombinant DNA contg. eukaryotic telomere esp. from higher plant - useful as vector for specific genes and maintained in nucleus as independent replicating molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide nucleic acid; PNA; HIV; human immunodeficiency virus; AIDS; antiviral; antisense; triple helix; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
"at least one (and preferably all) of
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 6; DB 10; Length 7; Best Local Similarity 100.0%; Pred. No. 3.7e+08; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide nucleic acid oligomer targetting HIV gene.
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7 BP; 3 A; 3 C; 0 G; 1 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                 Claim 35; page 50; 65pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ97993 standard; DNA; 8 BP.
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                                                                                                                                         88US-0172467.
                                                                                                         89WO-US00795.
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(first entry)
                                                                                                                                                                      (GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                      Richards E, Ausubel FM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag=
/note=
              Arabidopsis thaliana.
                                                                                                                                                                                                                                   WPI; 1989-309497/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TTAGGG 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTAGGG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                         27-FEB-1989;
                                                                                                                                         24-MAR-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2003
19-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-FEB-1995.
                                            WO8909219-A.
                                                                           05-0CT-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ97993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tandem repeats (1-1000) of the telomere are used in a vector for expressing specific genes in plants. They provide 'artificial chromosomes' which are maintained in the nucleus, so are not subjected to variable expression due to integration-position effects. They allow the integration of very foreign DNA without host range limitations. The telomere opt. contains variant repeats of CTCTAAA. The telomere is pref. the pAtT4 plasmid (ATCC 67577). (Updated on 25-WAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Variant telomere; Arabidopsis thaliana; vector; artificial chromosomes;
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New recombinant DNA contg. eukaryotic telomere esp. from higher plant - useful as vector for specific genes and maintained in nucleus as independent replicating molecule.

88US-0172467. 89WO-US00795

24-MAR-1988; 27-FEB-1989;

(GEHO ) GEN HOSPITAL CORP.

axxxaax**aaxaaaaaaaaaaaaa**a**xaaaaaayyyyy** 

Richards E, Ausubel FM;

WPI; 1989-309497/42.

Claim 28; page 50; 65pp; English.

Telomere; Arabidopsis thaliana; vector; artificial chromosomes;

Arabidopsis thaliana.

WO8909219-A. 05-OCT-1989

tandem repeat

relomere of Arabidopsis thaliana.

(updated)
(first entry)

25-MAR-2003 22-FEB-1990

AAN91439;

AAN91439/c ID AAN91439 standard; DNA; 7 BP.

RESULT 6

|||||| 1 TTAGGG (

Gaps

; 0

100.0%; Score 6; DB 10; Length 7; 100.0%; Pred. No. 3.7e+08; trive 0; Mismatches 0; Indels

6; Conservative

1 TTAGGG 6

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Local Similarity

Best Loc Matches

Query Match

Variant of Arabidopsis thaliana telomere.

tandem repeat

(updated)
(first entry)

25-MAR-2003 22-FEB-1990

AAN91442;

AAN91442 standard; DNA; 7 BP

AAN91442/c

RESULT 7

Sequence 7 BP; 3 A; 3 C; 0 G; 1 T; 0 other;

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Gaps

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Matches

g ઢ

SXS

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Melanogenesis associated oligonucleotide #12.
                                                                                                                                                                                Claim 1; Page 37; 74pp; English.
          AAS14916 standard; DNA; 6 BP.
                                                                                                                       31-MAR-2000; 2000US-0540843.
                                                                                                             30-MAR-2001; 2001WO-US10162.
                            (first entry)
                                                                                                                                         Gilchrest BA, Yaar M,
                                                                                                                                                    WPI; 2001-626338/72.
                                                                                                                                 (UYBO-) UNIV BOSTON
                                                                                           WO200174342-A2
                            14-FEB-2002
                                                                                                    11-OCT-2001
                                                                                 Synthetic
                   AAS14916;
     AAS14916,
RESULT 4
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sequence is melanogenesis associated oligonucleotide #12, the reverse complementary sequence of AAS149015, a truncated version of the sequence representing the telomere over-hang sequence (AAS14909), described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               incompetence in a cell line are useful for preventing a full term pregnancy in an animal and inhibiting totipotence. The molecules are also useful for treating a disease in an animal by inducing development of one or more cells of the animal into a specific cell type. The present sequence represents a bovine EST which is given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes an expressed sequence tag (EST), where the EST is an isolated, enriched, or purified nucleic acid sequence representing all or part of a gene, the expression of which, or its complementary sequence, in a cell identifies the cell as a developmentally competent or incompetent cell. Molecules which induce developmental competence in a cell line are useful for inducing totipotence in one or more cells. Molecules which induce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovine; Bos taurus; EST; expressed sequence tag; totipotence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         An expressed sequence tag (EST), the expression of which, complementary sequence, in a cell identifies the cell as a developmentally competent or incompetent cell -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovine embryonic germ (EG) cell cDNA EST 990913a CONTIG 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 6;
                                                                                                                                                                                                        Length 6;
                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                   100.0%; Score 6; DB 23; I
100.0%; Pred. No. 4.3e+08;
iive 0; Mismatches 0;
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100.0%; Pred. No. 4.3e+08;
ive 0; Mismatches 0;
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                                                                                                                                                Sequence 6 BP; 2 A; 3 C; 0 G; 1 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence 6 BP; 1 A; 0 C; 3 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 16; Page 210; 584pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eilertsen KJ, Pfister-Genskow M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABN73654 standard; cDNA; 6 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-2000; 2000US-209874P.
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                                                                                                                                                                                                                                                              6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       development; gene; ss.
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Best Local Similarity
                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                      1 TTAGGG 6
                                                                                                                                                                                                                                                                                                                                                                           TTAGGG 1
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                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
ABN73654
     8888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention describes inhibition of mammalian epithelial cell

proliferation by treating cells with at least one oligonucleotide, or

the fragment. The compounds, which have cytostatic, anti-apsoriatic and

anti-inflammatory, dermatological, ophthalmological, anti-apsoriatic and

inmunosuppressive activities, function as 'ultra-violet mimics' to induce

constant processes (or a protective response to later exposure to

radiation or chemicals), as a proliferation inhibitor, apoptosis inducer

or a tumour necrosis factor inhibitor. Probably they mimic products of

DNA damage, or processed DNA-damage intermediates, by inducing the p53

pathway, resulting in transient arrest of cell growth, allowing more time

for DNA repair to occur before cell division takes place. The method is

pathway, resulting in transient arrest of cell growth, allowing more time

for DNA repair to occur before cell division takes place. The method is

pathway, resulting in transient arrest of cell growth, allowing more time

for DNA repair to occur before cell division takes place. The method is

capecially used to treat carcinoma but may also be used to: treat other

hyperproliferative states (e.g. psoriasis or precancerous conditions);

reduce photoadang, oxidative stress or damage; prevent skin cancer; treat

allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in

cells caused by radiation or chemicals; increase melanin production

cells caused by radiation or chemicals; increase melanin production

promote apoptosis in epithelial cells (e.g. for treating vitiligo), and to

promote apoptosis in epithelial cells that contain damaged DNA. Also

oligonucleotides that contain non-hydrolyzable backbones are used to

inhibit apoptosis, in response to DNA damage, in epithelial cells that
                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Melanin, melanogenic; oligomer; cytostatic; anti-allergic; p53; anti-inflammatory; dermatological; ophthalmological; anti-psoriatic; immunosuppressive; DNA repair; proliferation inhibitor; apoptosis; tumour necrosis factor inhibitor; photoaging; hyperproliferative disease; carcinoma; oxidative stress; skin canoer; allergy mediated inflammation; conjunctivitis; allergic rhinitis; vitiligo; ss.
epithelial cell proliferation, described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inhibiting proliferation of epithelial cells, useful e.g. for treating carcinoma, using specific oligonucleotides that mimic the effects of ultra-violet light -
                                                                                                                                                                           Gaps
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                                                                                                                   Length 6;
                                                                                                                                                                        0; Indels
                                                                                                             100.0%; Score 6; DB 23; I
100.0%; Pred. No. 4.3e+08;
ive 0; Mismatches 0;
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                                                                                                       Query Match
Best Local Similarity
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Gaps

The representation of the representation of

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Increasing telomere length in cells - to increase proliferative capacity and therefore delay cellular senescence, useful in cell
                                                                                                therapy and transplantation
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Claim 12; Page 29; 38pp; English.

Oligonucleotides AATO5734-7 are examples of telomerase substrates used to increase the proliferative capacity of normal cells that express telomerase activity. The oligonucleotides allow an increase in length of telomeres in normal cells and in hybrids of normal and immortalised cells. The increase in telomere length extends the capacity of cells to replicate, esp. those treated ex vivo and used for transplantation techniques e.g. cell therapy, for the treatment of AIDS, anaemia, leukaemia or lymphoma.

Sequence 6 BP; 1 A; 0 C; 3 G; 2 T; 0 other;

Gaps ö 100.0%; Score 6; DB 16; Length 6; 100.0%; Pred. No. 4.3e+08; tive 0; Mismatches 0; Indels 6; Conservative Best Local Similarity Query Match Matches

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TTAGGG

AAX80998 standard; DNA; 6 BP.

AAX80998;

13-SEP-1999 (first entry)

Telomeric repeat sequence

Telomerase reverse transcriptase; TERT; mouse; telomere length assay; immunogen; enzyme; telomerase-mediated DNA replication; human; ss.

Homo sapiens

WO9927113-A1

03-JUN-1999

98WO-US25211 25-NOV-1998;

98US-0042460. 97US-0979742 16-MAR-1998; 26-NOV-1997;

(YESH ) UNIV YESHIVA EINSTEIN COLLEGE. (GERO-) GERON CORP

Greenberg R, Morin GB Allsopp R, Depinho R,

WPI; 1999-347722/29

Mouse telomerase reverse transcriptase (mTERT) enzyme proteins and nucleic acids

Disclosure, Page 62; 135pp; English.

The invention relates to a mouse telomerase reverse transcriptase (mTERT) assays. Compositions containing mTERT can be used in telomere length assays. Isolated mTERT is useful as an immunogen for the production of monoclonal or polyclonal antibodies. The method is useful for assessing the degree of purification and identification of new mTERT species, such as an mTERT allele, homolog or isoform, or to screen for medulators (antagonists and agonists) of telomerase-mediated DNA replication. Antagonists and agonists of mTERT can be used to modify the activity of other telomerase enzymes such as human TERT (hTERT).

Sequence 6 BP; 1 A; 0 C; 3 G; 2 T; 0 other;

ö Melanin, melanogenic; oligomer; cytostatic; anti-allergic; p53; anti-inflammatory; dermatological; ophthalmological; anti-psoriatic; anti-inflammatory; dermatological; ophthalmological; anti-psoriatic; tumunosuppressive; DNA repair; proliferation inhibitor; apoptosis; tumour necrosis factor inhibitor; photoaging; hyperproliferative disease; carcinoma; oxidative stress; skin cancer; allergy mediated inflammation; conjunctivitis; allergic rhinitis; vitiligo; ss. Gaps ö Length 6; 0; Indels 100.0%; Score 6; DB 20; I 100.0%; Pred. No. 4.3e+08; Melanogenesis assocaited oligonucleotide #11. Mismatches .; 0 AAS14915 standard; DNA; 6 BP. (first entry) Best Local Similarity 100. Matches 6; Conservative 1 TTAGGG 6 14-FEB-2002 AAS14915; Query Match RESULT 3 AAS14915 g ò

30-MAR-2001; 2001WO-US10162. WO200174342-A2

Synthetic.

31-MAR-2000; 2000US-0540843 Gilchrest BA, Yaar M, (UYBO-) UNIV BOSTON

WPI; 2001-626338/72

Inhibiting proliferation of epithelial cells, useful e.g. for treating carcinoma, using specific oligonucleotides that mimic the effects of ultra-violet light

Claim 1; Page 37; 74pp; English.

proliferation by treating cells with at least one oligonuclectie, or proliferation by treating cells with at least one oligonuclectie, or anti-allergic, anti-inflammatory, dermatological, ophthalmological, anti-apportatic and immunosuppressive activities, function as 'ultra-violet mimics' to induce DNA repair processes (or a protective response to later exposure to radiation or chemicals), as a proliferation inhibitor, apoptosis inducer or a tumour necrosis factor inhibitor. Probably they mimic products of DNA damage, or processed DNA-damage intermediates, by inducing the p53 pathway, resulting in transient arrest of cell growth, allowing more time for DNA repair to occur before cell division takes place. The method is especially used to treat carcinoma but may also be used to: treat other hyperproliferative states (e.g. psoriasis or precancerous conditions); react reduce photoaging, oxidative stress or damage; prevent skin cancer; treat allergically mediated inflammation (atopic or contact dermatitis, allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in cells caused by radiation or chemicals; increase melanin production (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to promote apoptosis in epithelial cells that contain damaged DNA. Also Oligonucleotides that contain non-hydrolyzable backbones are used to inhibit apoptosis, in response to DNA damage, in epithelial cell. This sequence is melanogenesis associated oligonucleotide #11, a truncated version of the sequence representing the telomere over-hang sequence (AAS14909) and one of the oligonucleotides used to inhibit mammalian The invention describes inhibition of mammalian epithelial cell

us-09-540-843-11.szlm30.rng

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December 31, 2003, 11:36:21 ; Search time 173.392 Seconds (without alignments) 93.410 Million cell updates/sec
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Minimum DB seq length: 0

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Listing first 45 summaries
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Gaps ö PAT 22-JUN-2001

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0138577-A 1298 31-MAY-2001;
The Johns Hopkins University (US)
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0138577-A 1296 31-MAY-2001,
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Patent: WO 0138577-A 1297 31-MAY-2001,
The Johns Hopkins University (US)
Location/Qualifiers
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Patent: WO 0138577-A 92 31-MAY-2001;
The Johns Hopkins University (US)
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Unclassified.

I (bases 1 to 10)
Windle, B.E., Qiu, M., Chen, S.-F., Fletcher, T.M. and Maine, I.
Rapid and sensitive assays for detecting and distinguishing between.
processive and non-processive telomerase activities
Patent: US 5856096-A 10 05-UAN-1999;
Location/Qualifiers
                                                            PAT 29-SEP-1999
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Dases 1 to 10)
Cech.T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C.B. and Andrews,W.H.
Human telomerase catalytic subunit: diagnostic and therapeutic
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ilarity 100.0%; Pred. No. 5.3e+06;
Conservative 0; Mismatches 0:
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Patent: US 6475789-A 294 05-NOV-2002;
Location/Qualifiers
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Sequence 294 from patent US 6475789.
                                                            AR026485 10 bp I
Sequence 10 from patent US 5856096.
AR026485
AR026485.1 GI:5937325
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/organism="unknown"
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'desc = 'peptide nucleic acid (PNA), where (deoxy(ribose- CC
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JP 2001517929-A/16
09-0CT-2001
09-APR-1997 JP 1997536487
09-APR-1996 US 08/630019
JERRY W SHAY,WOODRING E WRIGHT,MIECZYSLAW A PIATYSZEK,DAVID
/note= 'N = 1-50 peptide nucleic acid nucleobases, selected from U, T, A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shay,J.W., Wright,W.E., Piatyszek,M.A., Corey,D. and Norton,J.C. Modulation of mammalian telomerase by peptide nucleic acids Patent: JP 2001517929-A 16 09-OCT-2001; GERON CORP
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Strandedness: Single;
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/organism="unidentified"
                                                                                                                                 /mol_type="genomic_DNA"
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CC C nucleotide bases via
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JP 2001517929-A/16.
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Strandedness: Single;
Topology: Linear;
/desc = 'peptide nucleic acid (PNA), where (deoxy(ribose- CC
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JP 2001517929-A/29
09-CCT-2001
09-APR-1997 JP 1997536487
09-APR-1996 US 08/630019
JERRY W SHAY, WOODRING E WRIGHT, MIECZYSLAW A PIATYSZEK, DAVID
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JP 2001517929-A/33
09-0CT-2001
09-APR-1997 JP 1997536487
09-APR-1996 US 08/630019
JERRY W SHAY, WOODRING E WRIGHT, MIECZYSLAW A PIATYSZEK, DAVID
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Shay,J.W., Wright,W.E., Piatyszek,M.A., Corey,D. and Norton,J.C.
Modilation of mammalian telomerase by peptide nucleic acids
Patent: JP 2001517929-A 33 09-OCT-2001;
GERON CORP
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Modulation of mammalian telomerase by peptide nucleic acids.
BD071067
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CC cc nucleotide bases via glycine amino N through a CC
CC nucleotide bases via glycine amino N through a CC
CC /mod bases OTHER
CC /note = 'N = 1-50 peptide nucleic acid nucleobases,
CC / note = 'N = 1-50 peptide conclusion cc
from U, T, A,
CC G, i or C
CC G, i or C
/mod base = OTHER
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CC to nucleotide bases via glycine amino N through a methylenecarbonyl linker'
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100.0%; Pred. No. 5.1e+09;
ive 0; Mismatches 0;
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/organism="unidentified"
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Strandedness: Single;
Topology: Linear;
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/mod_base= OTHER
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linkages are replaced by N-(2-aminoethyl)glycine units linked
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Strandedness: Single;
Topology: Linear;
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JP 2001517929-A/15
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09-ACCT-2001
09-APR-1996 US 08/630019
09-APR-1996 US 08/630019
CORRY, WOODRING E WRIGHT, MIECZYSLAW A PIATYSZEK, DAVID JAMES C NORTON
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Shay, J.W., Wright, W.E., Piatyszek, M.A., Corey, D. and Norton, J.C. Modulation of mammalian telomerase by peptide nucleic acids Patent: JP 2001517929-A 29 09-OCT-2001;
GERON CORP
                                                                                                                                                                                                                             Shay,J.W., Wright,W.E., Piatyszek,M.A., Corey,D. and Norton,J.C. Modulation of mammalian telomerase by peptide nucleic acids Patent: JP 2001517929-A 15 09-OCT-2001; GERON CORP
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methylenecarbonyl linker'
FH Key Location/Qualifiers
I source 1.8
/organism='Unidentified'.
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/db_xref="taxon:32644"

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JP 2001517929-A/29.
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JP 2001517929-A/15.
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100.0%; Pred. No. 6.8e+09;
tive 0; Mismatches 0;
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100.0%; Pred. No. 6.8e+09;
tive 0; Mismatches 0;
                                       Score 6; DB 6; L
Pred. No. 6.8e+09;
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                                                                  0; Mismatches
                                                                                                                                                                                     Sequence 11 from Patent WO0174342. AX268763
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Sequence 12 from Patent WO0174342.
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Matches 6; Conservative
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synthetic construct
artificial sequences.

1 (bases 1 to 6)
Au,J.L. and Wientjes,G.
Compositions active in telomere damage comprising a taxane and
telomerase inhibitor
Patent: WO 0074667-A 10 14-DEC-2000;
Au, Jessie L.S. (US); Wientjes, Guillaume (US)
Locațion/Qualifiers
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1 (base 1 to 6)
Phillips,N.C. and Filion,M.C.
Therapeutically useful synthetic oligonucleotides
Patent: WO 0144465-A 49 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
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                                      /organism="synthetic construct"
/mol type="genomic DNA"
/db_xref="taxon:32630"
/note="synthetic primer"
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/db_wref="taxon:32630"
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Sequence 49 from Patent WO0144465.
AXI75285
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Location/Qualifiers
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December 31, 2003, 11:36:21 ; Search time 552.38 Seconds (without alignments) 444.364 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                             Gapop 10.0 , Gapext 1.0
Gapop 10.0 , Gapext 1.0
Searched: 2888711 seqs, 20454813386 residues

Oriotal number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Aximum DB seq length: 30
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 46 summarise
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9980559 on 05/19/2004
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synthetic construct
synthetic construct
artificial sequences.

1 (bases 1 to 6)
Hahn, W.C. and Weinberg, R.A.
Creation of human tumorigenic cells and uses therefor
Patent: WO 0073420-A 5 07-DEC-2000;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; DANA-FARBER 6 bp Sequence 5 from Patent W00073420. AX055801.1 GI:12228914 RESULT 1
AXO55801/c
LOCUS
DEFINITION
ACCESSION
VERSION
VERSION
CETYWORDS
SOURCE
ORGANISM REFERENCE AUTHORS TITLE JOURNAL is the number of results predicted by chance to have a

Pred. No.

PAT 13-JAN-2001

linear

DNA

ALIGNMENTS

BD071054 Modulatio BD071062 Modulatio BD171081 Human liv E36980 Human telom AR016034 Sequence AR026486 Sequence AR0549195 Sequence AR075506 Sequence AR114804 Sequence AR214804 Sequence AR310476 Sequence AR310450 Sequence AR368751 Sequence AX268761 Sequence AX268761 Sequence AX268761 Sequence AX383296 Sequence AX3834462 Sequence AX384462 Sequence AX394499 Sequence AX394499 Sequence AX394499 Sequence AX33440 Sequence Modulatio Modulatio Modulatio Modulatio Human tel Method fo Sequence Sequence Modulatio Sequence **Aodulatio** Sequence Sequence Sequence Sequence Sequence Seguence AX624942 Sequence score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. BD071067 AR026485 AR026485 AR152177 AX153381 AX153383 AX153383 AX153383 AX153383 AX153383 AX153383 AX153383 AX153383 BD023724 BD071041 BD071045 BD071051 SUMMARIES BD071049 BD071063 BD071067 BD071051 BD071054 BD071062 BD167218 AR026486 AR026487 AR301476 PX624942 DB Query Match Length 100.0 Score Ñ. υ

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Search completed: January 1, 2004, 01:10:39 Job time : 234.165 secs

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APPLICANT: Abbott Laboratories
APPLICANT: Abbott Laboratories
APPLICANT: Laboratories
APPLICANT: Leonard, Amanda Eun-Yeong
APPLICANT: Huang, Yung-Sheng
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
FILE REPERENCE: 607. US. P4
CURRENT APPLICATION NUMBER: US 0/903,456
FILE REPERENCE: 607. US. P4
CURRENT FILING DATE: 2001-07-11
PRIOR PILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: US 09/624,670
PRIOR PILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: US 09/379,095
PRIOR PILING DATE: 1908-09-02
NUMBER: OF SEQ ID NOS: 122
NUMBER: OF SEQ ID NOS: 122
SEQ ID NO 93
SEQ ID NO 93
                                  APPLICANT: Huang, Yung-Sheng, APPLICANT: Huang, Yung-Sheng, APPLICANT: Peroira, Suzette L.
TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF FILE REPERENCE: 6407. US. P3
CURRENT APPLICATION NUMBER: US/09/903,456
CURRENT RILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US 09/624,670
PRIOR PILING DATE: 1999-08-23
PRIOR PILING DATE: 1999-08-23
PRIOR PILING DATE: 1999-09-02
NUMBER: OF SEQ ID NOS: 116
SOFTWARE: PRAESEQ FOR Windows Version 4.0
SEQ ID NO 93
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Leonard, Amanda Eun-Yeong
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; Sequence 93, Application US/10156911

; Publication No. US20030163845A1

; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ROUVIÈCE, Pierre E
APPLICANT: ROUVIÈCE, Pierre E
APPLICANT: Brostowicz, Patricia C
TITLE OF INVENTION: GENES AND ENZYMES FOR THE PRODUCTION OF ADIPIC ACID
TITLE OF INVENTION: INTERMEDIATES
FILE REPERENCE: BC-1001
CURRENT APPLICATION NUMBER: US/10/230,562
CURRENT APPLICATION NUMBER: 60/120,702
PRIOR APPLICATION NUMBER: 60/120,702
PRIOR PILING DATE: 1999-02-19
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Microsoft Office 97
SEQ ID NO 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Publication No. US20030104410A1

GENERAL INFORMATION:

APPLICANT: Mitthen, Michael

TITLE OF INVENTION: Human Microarray

TITLE OF INVENTION: Human Microarray

TITLE OF INVENTION WUMBER: US/10/098,263B

CURRENT APPLICATION WUMBER: 60/276,759

RIOR APPLICATION WUMBER: 60/276,759

PRIOR PELING DATE: 2001-01-16

NUMBER OF SEQ ID NOS: 131066

OSOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

ESQ ID NO 31016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: primer
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1 Similarity 82.4%; Pred. No. 1.6e+04;
14; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
US-09-903-456-93/c
; Sequence 93, Application US/09903456
; Patent No. US20020138974A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
                                                                                                                                                                                                                                               US-10-230-562-43
. Sequence 43. Application US/10230562
. Publication No. US20030113886A1
. GENERAL INFORMATION:
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9 GGAGGCATGCATGACGT 25
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Best Local Similarity 75.0°
Matches 15; Conservative
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G Best Local Similarity
Matches 14; Conservat
Matches 14; Conservat
Matches 14; Conservat
Matches 16; Conservat
Matches
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; ORGANISM: Homo sapien
US-10-098-263B-31016
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GENERAL INFORMATION:
APPLICANT: Rouviere, Pierre E.
APPLICANT: Rouviere, Pierre E.
APPLICANT: BAZOSTOWICZ, PALTICIA C.
TITLE OF INFERNION: GENES AND ENZYMES FOR THE PRODUCTION OF ADIPIC ACID INTERMEDIATES FILE REPERENCE: BC1001 US NA
CURRENT APPLICATION NUMBER: US/09/954,314
CURRENT APPLICATION NUMBER: 60/120,702
PRIOR RELING DATE: 1999-February-19
NUMBER OF SEC ID NOS: 49
SOFTWARE: Microsoft Office 97
SEQ ID NO 43
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                                                                                                      Length 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2034, Application US/09940185
Publication No. US20030096239A1
GENERAL INFORMATION:
APPLICANT: Gunderson, Kevin
APPLICANT: Chee, Mark
TILL OF INVENTION: Probes and Decoder Oligonucleotides
FILE REFERENCE: A-69605-1
CURRENT APPLICATION NUMBER: US/09/940,185
CURRENT APPLICATION NUMBER: US 60/227,948
PRIOR FILING DATE: 2000-08-25
PRIOR FILING DATE: 2000-08-25
PRIOR FILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 4768
SEQ ID NO 2034
LENGTH: 24
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US-09-940-185-2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 61.0%; Score 12.2; DB 11; Best Local Similarity 82.4%; Pred. No. 1.5e+04; Matches 14; Conservative 0; Mismatches 3;
                                                                                                           Score 12.2; DB 13;
Pred. No. 1.5e+04;
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Best Local Similarity 82.4%; Pred. No. 1.6e+04;
Matches 14; Conservative 0; Mismatches 3;
                                                                                                                                                                                           0; Mismatches
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Patent No. US20020127666A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 TGCATGCATTACGTACG 20
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ORGANISM: Artificial Sequence
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                                                                                                  Query Match 61.0%;
Best Local Similarity 82.4%;
Matches 14; Conservative
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                 US-10-245-805-21
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                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: GRAHAM, Michael Wayne
APPLICANT: RICE, Robert No. US20030182672Alman
APPLICANT: REE, Rohert No. US20030182672Alman
APPLICANT: REED, Kenneth Clifford
APPLICANT: MURPHY, Kathleen Margaret
APPLICANT: Benitec Australia Ltd
APPLICANT: Benitec Australia Ltd
APPLICANT: Benitec Australia Ltd
APPLICANT: The State of Queensland through its Department of Primary Industries
TITLE OF INVENTION: GENETIC SILENCING
FILE REFERENCE: 546322000200
CURRENT APPLICATION NUMBER: PCT/AU01/00297
CURRENT FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
PRIOR PILING DATE: 2000-03-17
PRIOR PILING DATE: 2000-03-17
PRIOR PILING DATE: 2000-03-17
PRIOR PILING DATE: 2000-03-17
PRIOR PELING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 25
GOFFWARE: FastSEQ for Windows Version 4.0
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21 ATGCATGCTTTCCATAC 4

22 ATGCATGCTTTCCATAC 4

23 SEQUENCE 21, Application US/10245805

24 Sequence 21, Application US/10245805

25 SEQUENCE 21, Application US/10245805

26 SEQUENCE 21, Application US/10245805

27 SEQUENCE 21, Application US/10245805

28 PRICANT: GRAHAM, Michael Wayne

APPLICANT: REED, Kenneth Clifford

APPLICANT: REED, Kenneth Clifford

APPLICANT: Benitec Australia 1rd

APPLICANT: Benitec Australia 1rd

APPLICANT: The State of Queensland through its Department of Primary Industries

TILLE REFERENCE: 54632200020

CURRENT PILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: NS/10/245,805

CURRENT PILING DATE: 2000-03-17

PRIOR FILING DATE: 2000-03-17

PRIOR FILING DATE: 2000-03-17

PRIOR FILING DATE: 2001-03-17

SECOLO 21 NO PRIOR 25

NUMBER OF SEQ ID NOS: 25

SEO ID NO 21

SECOLO 21

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                                                                                                                                                                                                                                                                   ; Sequence 20, Application US/10245805; Publication No. US20030182672A1; GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
17 ATGCCTGCATTGTGTAC 1
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CURRENT FILIDE DATE: 2002-09
PRIOR APPLICATION NUMBER: UCO-09
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-17
PRIOR PILING DATE: 2001-03-17
PRIOR PILING DATE: 2001-03-17
PRIOR PILING DATE: 2001-03-17
PRIOR PILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 25
SOFTWARR: FARLSEQ for Windows SEQ ID NO 20
LENGTH: 23
TYPE: DNA
ORGANISM: Artificial Sequence
PRATURE:
OTHER INFORMATION: Double St: CRATURE:
OTHER INFORMATION: C
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US-10-245-805-20/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Human DNA Mismatch Repair Proteins FILE REFERENCE: PF106P3D1
CURRENT APPLICATION: Human DNA Mismatch Repair Proteins; FILE REFERENCE: PF106P3D1
CURRENT FILING DATE: 1002-02-22
PRIOR APPLICATION NUMBER: PCT/US95/01035
PRIOR FILING DATE: 1995-01-25
PRIOR FILING DATE: 1995-06-06
PRIOR FILING DATE: 1995-06-06
PRIOR FILING DATE: 1995-06-06
PRIOR PLING DATE: 1994-08-06
PRIOR PLING DATE: 1994-08-06
PRIOR PLING DATE: 1994-08-06
PRIOR PLING DATE: 1994-08-23
PRIOR FILING DATE: 1994-03-16
PRIOR FILING DATE: 1994-03-16
PRIOR FILING DATE: 1994-03-16
PRIOR PLING DATE: 1994-03-16
                                                                                                                                                                                                                                                                                                           APPLICANT: International Paper Co.
APPLICANT: Echt, Craig. S
APPLICANT: Nelson, c. Dana
TITLE.OF INVENTION: MICROSATELITE DNA MARKERS AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 4481/IE188US1
CURRENT APPLICATION NUMBER: US/09/232,785
CURRENT FILING DATE: 1999-01-19
FRIOR APPLICATION NUMBER: 09/232,884
PRIOR FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 397
SOFTWARE: FastSEQ for Windows Version 3.0
SSET ID NO 139
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTHER INFORMATION: hMLH1 sense primer US-10-079-429-21
                                                                                                                                                                          US-09-232-785-139
; Sequence 139, Application US/09232785
; Publication No. US20030049612A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21, Application US/10079429 Publication No. US20030027177A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 TGCATGCATTACGTACG 20
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 82.4
Matches 14; Conservative
13 GCATGCATGCATT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Haseltine et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA; ORGANISM: Pinus taeda L. US-09-232-785-139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
US-10-079-429-21/c
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FILE REFERENCE: 429-63317

CURRENT FILING DATE: 2002-07-19

PRIOR PEDICATION NUMBER: US 60/176,115

PRIOR APPLICATION NUMBER: US 60/176,115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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Pred. No. 2.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 65.0%; Score 13; DB 13; Length 17; Best Local Similarity 100.0%; Pred. No. 6e+03; Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                           APPLICANT: Glichest, Barbara A.

APPLICANT: Glichest, Mark S.

APPLICANT: Eller, Mark S.

APPLICANT: Eller, Mark S.

TITLE OF INVENTION: Method to Inhibit Cell Growth Using TITLE OF INVENTION: Oligonucleotides FILE REFERENCE: 0054-1088-018/10/122,633

CURRENT PRILIAG DATE: 2002-04-12

PRIOR APPLICATION NUMBER: US 09/540,843

PRIOR PLILING DATE: 2000-03-31

PRIOR PLILING DATE: 2000-03-31

PRIOR PLILING DATE: 2000-03-31

PRIOR PLILING DATE: 2001-03-30

DATE: AND APPLICATION NUMBER: PCT/US01/10162

DATE: AND APPLICATION NUMBER: PCT/US01/10162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GS-10-194-035-95/c
JN Sequence 95, Application US/10194035
Publication No. US20030144229A1
1 GCATGCATGCATTACGTACG 20
                                                                                                                                                                          US-10-122-633-8
; Sequence 8, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PE: DNA
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3 ATGCATGCATTACGTAC 19

1 GCATGCATGCATT 13

Sequence 12, Appl Sequence 14, Appl Sequence 20, Appl Sequence 21, Appl

Sequence Sequence

Appli

14, Appl 55338, A 120655, 15, Appl

Sequence Sequence

Seguence Sequence

ALIGNMENTS

Sequence Sequence Sequence

Sequence 1 Sequence 1 Sequence 5

Sequence 97436, A Sequence 97803, A Sequence 105971,

5 US-10-098-263B-60894
5 US-10-098-263B-69160
1 US-09-957-483B-69160
1 US-09-957-483B-69160
1 US-09-957-483B-69160
5 US-10-118-495-14
5 US-10-118-495-14
5 US-10-118-495-14
6 US-09-833-605-4
0 US-09-833-605-4
0 US-09-833-605-4
0 US-09-833-605-4
0 US-09-823-8574
5 US-10-098-263B-30574
5 US-10-098-263B-30574
5 US-10-098-263B-30574
6 US-10-098-263B-37436
7 US-10-168-445-112
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0 US-10-194-035-95

Sequence 35044, Sequence 30574, Sequence 30573, Sequence 4, Ap Sequence 11,

Sequence 4, Appli Sequence 112, App Sequence 153, App

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US-10-122-630-8
                                                                                                                   (without alignments)
296.896 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                  December 31, 2003, 17:10:00 ; Search time 233.165 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                            Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
          GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                 Gapop 10.0, Gapext 1.0

Gapop 10.0, Gapext 1.0

Gapop 10.0, Gapext 1.0

Gapop 10.0, Gapext 1.0

Z263443 seqs, 1730637950 residues

Grotal number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum Match 08

Gost-processing: Minimum Match 1008

Harimum Match 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-122-630-8
US-10-122-633-8
US-10-134-035-95
US-09-232-785-139
US-10-245-805-20
US-10-245-805-20
US-09-940-185-2034
US-09-940-185-2034
US-09-954-314-43
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Listing first 45 summaries
                                                                      nucleic search, using sw model
                                                                                                                                                                                            1 gcatgcatgcattacgtacg 20
                                                                                                                                                                                                                      IDENTITY NUC Gapoxt 1.0
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20
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Match Length
                          Copyright
                                                                                                                                                                           Perfect score:
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                                                                                                                                                                                            Sequence:
                                                                                                   Run on:
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No.
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Gaps
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                                                                                                            APPLICANT: B11cr, Mark S.
APPLICANT: B1cr, Mark S.
APPLICANT: B1cr, Mark S.
APPLICANT: Yaar, Mina
TITLE OF INVENTION: Oligomucleotides
TITLE OF INVENTION: Oligomucleotides
TITLE OF INVENTION: Oligomucleotides
CURRENT PLING DATE: 0054.1088-018
CURRENT PLING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: US 08/467,012
PRIOR FILING DATE: 1995-06-06
PRIOR FILING DATE: 1996-06-03
PRIOR FILING DATE: 1996-06-03
PRIOR FILING DATE: 1996-06-03
PRIOR FILING DATE: 1996-06-03
PRIOR FILING DATE: 2000-03-11
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-31
PRIOR PLING DATE: 2001-03-31
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100.0%; Score 20; DB 15;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Synthetic DNA Fragment
Sequence 8, Application US/10122630; Publication No. US2030032610A1; GENERAL INFORMATION: APPLICANT: Gilchrest, Barbara A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JS-10-122-630-8
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1 GCATGCATGCATTACGTACG 20

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43, Appl 31016, A 43, App

US-10-098-263B-31016

US-09-903-456-93 US-10-156-911-93 US-10-408-736-66 US-09-940-185-3327

Sequence Sequence Sequence

Sequence

Sequence Sequence Sequence Sequence Sequence Sequence Sequence

Sequence

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COMPUTER LEADER STREET: 633 West Fifth Street
STATE: California
COUNTRY: 108 Angeles
STATE: California
COUNTRY: 108 Angeles
STATE: California
COUNTRY: 108 Angeles
STATE: California
COMPUTER READER FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: STATE: 12 Mc Compatible Country
COMPUTER: 1.50 DATE: 1.50 DATE
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58.0%; Score 11.6; DB 3; Length 20; 77.8%; Pred. No. 2.8e+03; Live 0; Mismatches 4; Indels
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Sequence 3. Application US/09724753
Patent No. 6416953
GENERAL INFORMATION:
GENERAL INFORMATION:
SELF-ORGANIZING MOLECULAR PHOTONIC
TITLE OF INVENTION: SELF-ORGANIZING MOLECULAR PHOTONIC
STRUCTURES BASED ON CHROMOPHORE-
AND FLUOROPHORE-CONTAINING
POLYNUCLEOTIDES AND METHODS OF
                                                                                                                                                                                             TITLE OF INVENTION: SELF-ORGANIZING MOLECULAR PHOTONIC TITLE OF INVENTION: STRUCTURES BASED ON CHROMOPHORE-TITLE OF INVENTION: TOTAL STRUCTURES AND METHODS OF TITLE OF INVENTION: POLYNUCLEOTIDES AND METHODS OF TITLE OF INVENTION: THEIR USE CORRESPONDENCE: 11

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: 1BM COMPALIAble
OPERATING SYSTEM: 1BM P.C. DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION WUMBER: US/09/123,638
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/703,601
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                    Sequence 3, Application US/09123638 Patent No. 6162603
                                                                                                                                                                                                                                                                                                                                                                                                  E: Lyon & Lyon
633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 ATGCATGCATTACGTACG 20
                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Michael J. Heller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 77.8
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Los Angeles
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
STREET: 63
                          RESULT 14
US-09-123-638-3/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-724-753-3/c
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0
                                                                                                                                                                  58.0%; Score 11.6; DB 1; Length 20; 77.8%; Pred. No. 2.8e+03;
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                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application Us/08703601
Patent No. 5849469
GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE OF INVENTION: SELF-ORGANIZING MOLECULAR PHOTONIC TITLE OF INVENTION: STELF-ORGANIZING MOLECULAR PHOTONIC TITLE OF INVENTION: AND FLUOROPHORE-CONTALINING TITLE OF INVENTION: POLYNUCLEOTIDES AND METHODS OF TITLE OF INVENTION: THEIR USE NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CALF: 570.7

COMPUTER READALE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: 1BM Compatible
OPERATURG SYSTEM: 1BM P.C.
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 02/08/703,601
FILING DATE: August 23, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/232,233
FILING DATE: May 5, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Kannong John
                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Lyon & Lyon
633 West Fifth Street
                                                                                                                                                                                                                                                                                 3 ATGCATGCATTACGTACG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Kappos, John
REGISTRATION NUMBER: 37,861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 ATGCATGCATTACGTACG 20
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                             DNA (genomic)
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                                                                                                                                                                                       Best Local Similarity 77.8 Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 77.8
hes 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 633 West 1
CITY: Los Angeles
STATE: California
linear
                       MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ANTI-SENSE: NO
US-08-703-601-3
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Sequence 3, Appli
Category

Patent No. 584946
GENERAL INFORM
APPLICANT: N
TITLE OF INV
TITLE OF IN
                                                                                                           US-08-232-233-3
                                                                                                                                                                  Query Match
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Matches
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ADDRESSEE: Lyon & Lyon

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GENERAL INFORMATION:
APPLICANT: Michael J. Heller
TITLE OF INVENTION:
SELF-ORGANIZING MOLECULAR PHOTONIC
TITLE OF INVENTION:
STRUCTURES BASED ON CHROMOPHORE- AND FLUOROPHORE-
TITLE OF INVENTION:
CONTAINING POLYNUCLEOTIDES AND METHODS OF THEIR USE
NUMBER OF SEQUENCES:
11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
COMPUTER: IBM P.C. DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,233
FILING DATE: May 4, 1994
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 07/790,262
FILING DATE: No. 5565322ember 7, 1992
ATTORNEY/AGENT INFORMATION:
                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/790,262
FILING DATE: 07-00v-1991
ATTORNEY AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFECOMMUNICATION INFORMATION:
TELEPHONE: 619-792-3680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Murphy, David B.
REGISTRATION NUMBER: 31,125
REFERENCE/DOCKET NUMBER: 207/170
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELERA: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR EEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-232-233-3/c
, Sequence 3, Application US/08232233
, Patent No. 5565322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Lyon & Lyon
611 West Sixth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 ATGCATGCATTACGTACG 20
                                                                                                                                                                                                                                                                               TELEFAX: 619-792-8477
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 ATGCATACGTTCAGTACG 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
R: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 77.8
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 611 mec.
CITY: Los Angeles
cTATE: California
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: 1:
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STATE: CE
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-250-951-3
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US-14-14-18-18-4-28.

GENERAL INFORMATION:

APPLICANT: Mukerji, Pradip

APPLICANT: Mukerji, Pradip

APPLICANT: Mukerji, Pradip

APPLICANT: Thurmond, Jennifer

APPLI
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                       OTHER INFORMATION: Description of Artificial Sequence: unknown US-09-134-855-1
                                                                                                                 Length 15;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/250,951
FILING DATE:
                                                                                                           Query Match 60.0%; Score 12; DB 3; L¢
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 12; Conservative 0; Mismatches 0;
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  ; FEATURE:
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APPLICANT: CHOUDEARY, Gargi
APPLICANT: CHOUDEARY, Gargi
APPLICANT: HAHNENBERGER, Karen
APPLICANT: HOUDEARY, Philip J
APPLICANT: LICHTENWALTER, Kay
APPLICANT: LICHTENWALTER, Kay
APPLICANT: LICHTENWALTER, Kay
APPLICANT: HANCOCK, William S
TITLE OF INVENTION: (As Amended) Method of Binding a Plurality of Chemicals
TITLE OF INVENTION: (As Amended) Method of Binding a Plurality of Chemicals
TITLE OF INVENTION: (As Amended) Method of Binding a Plurality of Chemicals
TITLE OF INVENTION: (As Amended) Method of Binding a Plurality of Chemicals
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TITLE OF INVENTION: (As Amended) Method of Binding a Plurality of Chemicals
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TITLE OF INVENTION: (As Amended) Method of Binding a Plurality of Chemicals
TITLE OF INVENTION: (As Amended) Method of Binding a Plurality of Chemicals
TITLE OF INVENTION: (As Amended) Method of Binding a Pluralit
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APPLICANT: CHOUDERRY, Gargi
APPLICANT: CHOUDERRY, Karen
APPLICANT: WICKES, Philip J
APPLICANT: WICKES, Philip J
APPLICANT: LICHTENWALTER, Kay
APPLICANT: LICHTENWALTER, Kay
APPLICANT: HANCOCK, William S
TITLE OF INVENTION: (As Amended) Method of Binding a Plurality of Chemicals
TITLE OF INVENTION: on a Substrate by Electrophoretic Self-Assembly
FILE REPERBNCE: 5000-0050
CURRENT APPLICATION NUMBER: US/09/134,855
CURRENT FILING DATE: 1998-08-14
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Batentin Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.0%; Score 12; DB 3; Length 15;
100.0%; Pred. No. 1.70+03;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: modified_base
LOCATION: (1)
FFATURE:
NAME/KEY: modified_base
LOCATION: (1)
OTHER INFORMATION: n is 2' fluorodeoxycytidine
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LOCATION: (1)
OTHER INFORMATION: n is 2' fluorodeoxycytidine
                                                                                                                                                                                                                US-09-134-855-1
; Sequence 1, Application US/09134855
; Patent No. 6107038
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        9 GGAGGCATGCATGACGT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GCATGCATGCAT 12
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NAME/KEY: modified_base
LOCATION: (1)
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                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
US-09-134-855-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-134-855-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 15
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GENERAL INFORMATION:
APPLICANT: Brzostowicz, Patricia C.
TITLE OF INVENTION: GENES AND ENZYMES FOR THE PRODUCTION OF ADIPIC ACID INTERMEDIATES
TITLE OF INVENTION UNMBER: US/09/954,314
CURRENT FILING DATE: 2001-09-17
FRIOR FILING DATE: 1999-February-19
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ROUGER, Pierre E. APPLICANT: Brostowicz, Patricia C. TILLE OF INVENTION: GENES AND ENZYMES FOR THE PRODUCTION OF ADIPIC ACID INTERMEDIATES FILE REFERENCE: BC1001 US NA CURRENT APPLICATION NUMBER: US/09/504,358
CURRENT APPLICATION NUMBER: G0/120,702
EARLIER PILING DATE: 2000-02-15
EARLIER PILING DATE: 1999-February-19
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Microsoft Office 97
SEQ ID NO 43
LENGTH: 30
TYPE: DA
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APPLICANT: ROUVIECE, Pierre E.

APPLICANT: ROUVIECE, Patricia C.

TILE REFERENCE: B.C1001 US NA

TILE REFERENCE: B.C1001 US NA

CURRENT FILING DATE: 1999-February-19

CURRENT FILING DATE: 1999-February-19

CURRENT FILING DATE: 1999-February-19

NUMBER OF SEQ ID NOS: 49

SOFTWARE: Microsoft Office 97

SEQ ID NO 43

LENGTH: 30

CHER INFORMATION: Description of Artificial Sequence: primer of Sequence of Properties of Particial Sequence of Properties of Particial Sequence of Particia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: primer US-09-954-314-43
                                                                                                                                                                               Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 30;
                                                                                                                                                                  Query Match 61.0%; Score 12.2; DB 4; Length 2 Best Local Similarity 82.4%; Pred. No. 1.4e+03; Matches 14; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 61.0%; Score 12.2; DB 4; Best Local Similarity 82.4%; Pred. No. 1.4e+03; Matches 14; Conservative 0; Mismatches 3;
; FEATURE: ; OTHER INFORMATION: hMLH1 sense primer US-08-187-757D-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 43, Application US/09504358
Patent No. 6365376
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                     3 ATGCATGCATTACGTAC 19
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US-09-504-358-43
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                                                                                                                                                                                                                                                                                                                                                                                                     61.0%; Score 12.2; DB 4; Length 20; 82.4%; Pred. No. 1.4e+03; Live 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Haseltine et al.
TITLE OF INVENTION: Human DNA Mismatch Repair Proteins
FILE REFERENCE: PF106F3
CURRENT APPLICATION NUMBER: US/08/468,024B
CURRENT TILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: 08/294,312
PRIOR APPLICATION NUMBER: 08/210,143
PRIOR FILING DATE: 1994-03-16
PRIOR PELING DATE: 1994-03-16
PRIOR FILING DATE: 1994-03-16
PRIOR FILING DATE: 1994-03-16
SROFWARE: PALENTIN NUMBER: 08/187,757
PRIOR FILING DATE: 1994-03-16
SOFTWARE: PALENTIN VONSER: 08/187,757
NUMBER: OS SOFTWARE: PALENTIN VONSER: 08/187,757
SOFTWARE: PALENTIN VONSER: 08/187,757
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Patent No. 6482606
GENERAL INFORMATION:
APPLICANT: Adams et al.
TITLE OF INVENTION: Human DNA Mismatch Repair Proteins
FILE REFERENCE: PF106
CURRENT APPLICATION NUMBER: US/08/187,757D
CURRENT FILING DATE: 1994-01-27
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTHER INFORMATION: hMLH1 sense primer US-08-468-0248-21
                                                                                                                                                                                                                                                                                                           COTHER INFORMATION: hMLH1 sense primer US-08-294-3128-21
PRIOR FILING DATE: 1994-03-16
PRIOR APPLICATION NUMBER: 08/187,757
PRIOR FILING DATE: 1994-01-27
WUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21, Application US/08468024B; Patent No. 6416984; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 Argcerscarrerac 1
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                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 82.44
Matches 14; Conservative
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                                                                                                                                                         SEQ ID NO 21
LENGTH: 20
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LENGTH: 21
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Sequence 21, Application US/08294312B
Fatent No. 6380369
GENERAL INCOMMATION:
TITLE OF INVENTION:
FILE REFERENCE: PF106EP;
FILE REFERENCE: PF106EP;
CURRENT ABLICATION NUMBER: US/08/294,312B
CURRENT FILING DATE: 1994-08-23
PRIOR APPLICATION NUMBER: 08/210,143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

COMPUTER: 13.5" Diskette, 1.44 Mb storage
COMPUTER: 18M PS/2 Model 502 or 55X
OPERATING SYSTEM: 18M P.C. DOS (Version 3.30)
SOFTWARE: 1891628
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/720,586
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 180404:
APPLICATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 193/121
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (1313) 616-04.00
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                                                                                                                                                                                                                                            Sequence 7, Application US/07720586
Patent No. 5232831
GENERAL INFORMATION:
APPLICANT: Curt Milliman
APPLICANT: Philip W. Hammond
TITLE OF INVENTION: TO STREPTOCOCCUS PYOGENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
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                                      CATGCATGCATTACG 16
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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TOPOLOGY: linear
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STATE: California
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US-07-720-586-7
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2218, App
763, App
5107, Ap
5108, App
18, Appl
4, Appl
14, Appl
34, Appl
34, Appl
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Sequence 4
Sequence 1
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APPLICANT: MOST, MASASHI
APPLICANT: OKUNO, TETSURO
APPLICANT: PURUSAMA, INMO
TITLE OF INVENTION: PROCESS FOR PRODUCTION OF
TITLE OF INVENTION: EXOGENOUS GENE OR ITS PRODUCT
TITLE OF INVENTION: IN PLANT CELLS NO.2
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                  US-09-001-826-13

US-08-687-421-55

US-09-264-854-13

US-09-371-7728-763

US-09-371-7728-5107

US-09-371-7728-5107

US-08-930-001-4

US-08-930-001-4

US-08-930-001-4

US-08-930-001-34

US-08-629-01A-34

US-08-629-01A-34

US-08-931-516-29

US-08-837-034-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
SOFTWARE: #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,564
FILING DATE: 28-APR-1993
                                                                                                                                                                                                                                                                                                                          US-08-944-974A-3
US-08-370-193A-6
US-07-884-811-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
DESCRIPTION: synthesized oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Sughrue, Mion, Zinn, Macpeak
                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 2100 Pennsylvania Avenue, N.W. Washington
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP HEI-4-152593
FILLING DATE: 28-APR-1992
TELECOMMUNICATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/08053564
Patent No. 5418153
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 bases
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Best Local Similarity 93.3
Matches 14; Conservative
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STATE: D.C.
COUNTRY: U.S.A.
TP: 20037
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  RESULT 1
US-08-053-564-10/c
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STREET: 21
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Appli
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                                                                                                                                            December 31, 2003, 14:40:05; Search time 77.7215 Seconds (without alignments) 113.581 Million cell updates/sec
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Grotal number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Asximum DB seq length: 30

Gost-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries
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US-07-720-586-7

US-08-468-024B-21

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US-08-10-15-15-19

US-08-10-13-19

US-09-134-855-1

US-09-134-855-1

US-09-134-855-1

US-09-145-028A-28

US-09-145-028A-28

US-09-145-028A-28

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US-09-145-028A-28

US-09-145-028A-28

US-09-123-631-3

US-08-250-951-3

US-08-2703-601-3

US-09-123-638-3

US-08-4773-3

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US-08-858-876A-12
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US-09-081-345-11
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US-09-601-943-3
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                                                                                                                                                                                                                                                                                                                            IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Plate: 0102 row: O column: 13 See primer: CACAGGAAACAGCTATGACC Class: plasmid ends High quality sequence stop: 30.

. .30 organism="Mus musculus" 'mol\_type="genomic DNA" 'strain="C57BL/6J" db\_xref="taxon:10090" /clone="UUGC2M0102013"

Location/Qualifiers

FEATURES

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(http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalot (gri #772114[gb]AP1290721); a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xiii0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Unun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
Mouse windle genome scaffolding with paired end reads from 10kb
plasmid inserts
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University of Utah Genome Center
University of Utah
Winiversity of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
                  /clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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Pred. No. 5.9e+05;
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91.7%;
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/clone l1b="Mouse 10kb plasmid UGCIM library"
/note="Vector: PWD42ry; Purified genomic DNA from M.
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                    Insert Length: 10000 Std Brror: (Plate: 0102 row: O column: 13 Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends
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                                                                                                                                                                                                                            /organism="Mus musculus"
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                                                                                                                                        High quality sequence stop: 30.
Location/Qualifiers
Email: ddunn@genetics.utah.edu
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91.7%;
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
University of Utah
Wm. 108, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Mouse_10kb_plasmid_UUGC2M_library"
//note="Vector: PWD42nv; Purified genomic_DNA_from M.musculus_C57BL/6J (female) was obtained from the Jackson laboratory Mouse_DNA_Resource
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       Plate: 0212 row: P column: 03
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 29.
Location/Qualifiers
                                                                                                                                                                                                                   organism="Mus musculus"
                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC, UT
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ZM0212P03R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0212P03 R, genomic survey sequence.
AZ949216
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Insert Length: 10000 Std Error: 0.00
Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends
                                                                                                                                                                               /organism="Mus musculus"
                                                                                                                                                                                                            /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="UUGC2M0212P03"
                                                                High quality sequence stop: 29.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                        /sex="Female"
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Decrease Control of Participation (Participation of Participation of Parti
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Gaps

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(http://www.jax.org/resources/
(http://www.jax.org/resources/
was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwlor (gf 147221141gb] AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Dunn,D., Aoyaqi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                          /lab host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42Iv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Insert Length: 10000 Std Error: 0.00
Plate: 0212 row: P column: 03
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                                                                                                                                                                               organism="Mus musculus"
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University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                   /mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0553F20"
                                             High quality sequence stop: 25.
Location/Qualifiers
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Mus musculus
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Email: ddunn@gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: Sal1; Site 2: Not1;
/note="Vector sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sal1-Not1, primer sites and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing granted in the context of the GABI-Beet project local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 25)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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                                             Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
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Insert Length: 10000 Std Error: 0.00
Plate: 0553 row: F column: 20
                                                                                                                                                                  Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 25 Std Error: 0.00
Plate: 17 row: K column: 24
Seq primer: T7; GTAATACGACTCACTATAGGGC.
Location/Qualifiers
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/clone="024-017-K24"
/tissue_type="storage root"
/lab_host="EMDH10B"
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organism="Beta vulgaris"
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Seg primer: CGTTGTAAAACGACGGCCAGT
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University of Utah Genome Center
University of Utah
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ADIS DNA core facility at MPIZ
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Fax: 801 585 7177
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Gaps

survey sequence.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 23)

Mus musculus (house mouse)

Mus musculus

ORGANISM

VERSION KEYWORDS SOURCE

REFERENCE AUTHORS

GI:12977531

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished

JOURNAL

COMMENT

TITLE

us-09-540-843-8.szlm30.rst

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb]AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into adaptored vector E oli KL10-Gold (stratagene) cells and selected for ampicillin resistance."
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BH907393 SALK 042093.38.75.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK 042093.38.75.x, genomic
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                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                        Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0
Plate: 0074 row: N column: 18
Seg primer: CACAGGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                High quality sequence stop: 23.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                               /clone="UUGC2M0074N18"
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91.7%;
                                                                                                                                                                                                                                                                                                                                                                                   /sex="Male"
                                                                                                                                                                                                              Class: plasmid ends
                                                                                            Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Conservative
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Rm. 308, Bi.
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BH907393
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Arabidopsis thallana
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 24)
Alonso,Ju., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
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Caryophyllales, Amaranthaceae; Beta.

(bases 1 to 25)

Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., prungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Contact: Weisshaar B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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E012713-024-017-K24-T7 MPIZ-ADIS-024-storage root Beta vulgaris
CDNA clone 024-017-K24 3-PRIME, mRNA sequence.
E0591292
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                                                                                                                                                                                                                                                                                                                                                                       Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Pax: 858 558 6379
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                                                                         Arabidopsis thaliana (thale cress)
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/strain="Columbia 0"
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Gaps

LOCUS

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Arabidopsis thaliana
Eukaryota; Viridiplaneae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 30)
Alonso,J.W., Leises,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C.J., Jeske,A., Karnes,W., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Ximmerman,J. and Ecker,J.R.
Arabidopsis Genome
Unpublished
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2M0074N18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0074N18 R, genomic survey sequence.
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                              53.0%; Score 10.6; DB 28; Length 28; 76.5%; Pred. No. 4.7e+05; ive 0; Mismatches 4; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
This Salk Institute for Biological Studies
Tolio N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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/mol type="genomic DNA"
/strain="Columbia 0"
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Location/Qualifiers
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BH910260
BH910260.1 GI:22723193
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                                                                Local Similarity 76.5
hes 13; Conservative
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                                                                                                                                                                                                                                                                                                                                GSS 04-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                       AZ477068 28 DA DNA linear GSS 04-OCT-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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                                                                   Gaps
                                                                   ö
   Score 11; DB 28; Length 20;
Pred. No. 2.9e+05;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                              clone UUGC1M0296B23 F, genomic survey sequence. AZ477068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0296 row: B column: 23
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 28.
Location/Qualifiers
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                                                             0; Mismatches
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/strain="C57BL/6J"
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/clone="UUGC1M0296B23"
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Mus musculus
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55.0%;
                                                                14; Conservative
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                                 Best Local Similarity
Matches 14; Conser
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AZ477068
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Gaps

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us-09-540-843-8.szlm30.rst

source

BASE COUNT ORIGIN

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/ Jab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/ Jab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/ Clone lib="Whouse loke plasmid UNGCIM library
/ Clone lib="Weator: PWD4Zuv; Purified genomic DNA from
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil 4772114 [gb] AF125072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                            AZ592714 20 bp DNA linear GSS 13-DEC-2000 1M0403P13R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0403P13 R, genomic survey sequence.
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Mus musculus
Mus musculus
Mus musculus
Mus accolus
Muscayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
                                 1; Indels
   Pred. No. 1.9e+05;
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                              0; Mismatches
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="UUGC1M0403P13"
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Location/Qualifiers
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AZ592714.1 GI:11714904
92.3%;
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                                                                                                                                                  2 CATCCATGCATTA 14
                                 12; Conservative
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Unpublished
   Best Local Similarity
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VERSION
KEYWORDS
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AUTHORS
                                 Matches
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AZ592714
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/lab_host="DH108"
/clone_lib="NCI CGAP_Pr28"
/note="Organ: prostate; Vector: pT773D-Pac (Pharmacia)
/note="Organ: prostate; Vector: pT773D-Pac (Pharmacia)
/note="Organ: prostate; Vector: plasmid DNA from the
normalized library NCI CGAP_Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NIC-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AIS68835 22 bp mRNA linear EST 13-APR-1999 th16912.xl NCI CGAP Pr28 Homo sapiens cDNA clone IMAGE:2118502 3' similar to WP:EEED8-8 CE01892 ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 22)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 985608-98679, 1101192-11011959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                Gaps
                              /organism= rock...
/db Arref="Faxon:9606"
/db Arref="Human adult lung 3' directed Mbol cDNA"
/note="Adult human lung, 3' directed Mbol"
/note="Adult human lung, 2' directed Mbol"
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                                                                                                                                                                                                                                                                Score 11.8; DB 14; Length 29; Pred. No. 1.4e+05; 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trace considered overall poor quality Insert Length: 1294 Std Error: 0.00 Seq primer: -40UP from Gibco High quality sequence scop: 1. Location/Qualifiers
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                           organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:2118502"
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                                                                                                                                                                                                                                                                   59.0%;
86.7%;
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                                                                                                                                                                                                                                                                                                                          13; Conservative
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Unpublished
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Best Local Similarity
Matches 13; Conserv
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57.0%; Score 11.4; DB 9; Length 22;

Query Match

BASE COUNT ORIGIN

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pMAQ2 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli xi10.Gold (Stratagene) cells and selected for ampicillin resistance."
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HUMGS03038 Human adult lung 3' directed Mbol cDNA Homo sapiens cDNA
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1 (bases 1 to 29)
1 (toh, K., Okubo, K., Yosii, J., Yokouchi, H. and Matsubara, K. An expression profile of active genes in human lung 5236275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_llb="Mouse_10kb plasmid UUGCNH library"
/note="Vector: PWD47nk; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Institute for Molecular and Cellular Biology
Osaka University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3-1, Yamadaoka, Suita, Osaka, 565, Japan
Tel: 06-877-5111 x3910
Fax: 06-877-1922.
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0; Mismatches 3
                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0298 row: E column: 16
Seq primer: CACACAGGAAACAGCTATGACC
Class: plaamid ends
High quality sequence stop: 26.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                               organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
/clone="UUGC1M0298E16"
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Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="Male"
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D45819
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      Fax: 801 585 7177
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TITLE
JOURNAL
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COMMENT
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D45819
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (http://www.jax.org/resource
(http://www.jax.org/resources/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMO42 (gil 4732114 |gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the innert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Wm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Milam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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1M0298E16R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0298E16 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab host="B. Coli strain XLIO-Gold, T1-resistant, F-"/clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0538 row: M column: 03
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                             organism="Mus musculus"
                                                                                                                                                                                                                                                                                                   'mol_type="genomic DNA"
'strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                            db_xref="taxon:10090"
clone="UUGC1M0538M03"
                                                                                                                                                                  High quality sequence stop: 27.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
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AZ478579.1 GI:10637573
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78.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="Male"
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Best Local Similarity

Matches 15; Conservat

An 2 CATGCATGCATT

2 CATGCATGCATT

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AUTHORS
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us-09-540-843-8.szlm30.rst

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Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurconathi; Muridae; Murinae; Mus.

1 (base 1 to 27)
1 slam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

L Unpublished

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84.112, USA
Tel: 801 585 5606
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                                                                       AZ810353 ZMO074018
BH907393 SALK 0420
BQ591292 E012713-0
AZ760021 IM0553F20
AZ949216 ZM0212P03
AZ846822 ZM0102013
AZ826822 ZM0102013
AZ826822 ZM0102013
AZ826822 ZM0102013
AZ826822 ZM0102013
AZ5800040 IM0338K07
AZ970807 ZM0248G20
AZ5700040 IM0338K07
AZ979817 ZM0248G20
AZ5700040 IM0338K07
AZ979817 ZM0248G20
AZ570040 IM0538M03
AZ3973185 AU013185
AU013203 AU013205
AZ952381 IM0464A02
AZ952381 IM0538M03
AZ013203 AU013205
AZ952824 IM0513405
AZ952327 ZM0213114
AZ796047 ZM0013405
AZ952327 ZM02131405
AZ952327 ZM02131405
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AZ424532 IM0513405
AZ424532 IM0513446
AU013568 AU013568
AZ335197 IM064K19
AZ435159 IM013668
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                               AZ477068
BH910260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                          AZ810353
BH907393
BC591292
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BH909058
AZ01332
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Mus musculus
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  December 31, 2003, 13:58:09 ; Search time 2297.97 Seconds (without alignments) 211.530 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33330
                     GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                Gapop 10.0, vapen....

Gapop 10.0, vapen....

Sarched: 22781392 seqs, 12152238056 residues

Frotal number of hits satisfying chosen parameters:

Ninimum DB seq length: 0

Aximum DB seq length: 30

Aximum Match 0%

Maximum Match 100%

Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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em_estin:
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em_gss_fun:,
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gb_gssl:*
gb_gss2:*
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29:
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Perfect score:
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5

JOURNAL

COMMENT

AZ660469 1M0538M03 AZ478579 1M0298E16 D45819 HUMGS03038 AI568835 th16g12.x

AZ660469 AZ478579 D45819 AI568835

28 178 9 4 6

24 25 25 25

63.0 61.0 59.0 57.0

12.6 12.2 11.8 11.8

4 2 C 4

Description

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DB

Length

Query

Score

Result No. υ

(INFE-) INFECTIO DIAGNOSTIC (IDI) INC.

Ouellette M; Boissinot M, Huletsky A, Menard C, Bergeron MG, Bolecter Roy PH;

WPI; 2001-245006/25

Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of algal, archaeal, bacterial, fungal and parasitical species in a test sample -

Claim 21, Page 1456; 1580pp; English.

The present invention describes a method for generating a repertory of nucleic acids of tuf, fus, atpD and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal, bacterial, fungal and parasitical species with a combination of defined primer pairs. The method can be used for producing probes and/or primers for detecting one or more related microorganisms e.g. algae, archaeal, bacterial, fungal and parasites, for universal detection and for specific and ubiquitous detection and identification of an algal, archaeal, bacterial, fungal and parasitical species, genus, family and group. A nucleic acid (I) obtained using the method of the invention can be used for the universal detection of any bacterium, fungus or parasite in a sample and for the detection of at least one antimicrobial agent resistance gene or at least one toxin gene. hack mucleic acids are used for the specific and ubiquitous detection and for identification of Streptococcus pneumoniae. (I) can be used to design a therapeutic agent which is effective against microorganisms. Macrobial species or genus or family or phylum or group which can be detected include Abiotrophia adiacens, Bordetella sp., Neisseria gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster results than substrate specificity tests as results can nucleotide sequences and primers/probes Corynebacterium sp., Enterobacteriaceae group, Escherichia coli, Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., determined in an hour and improved accuracy is also achieved. which are given in the exemplification of the present invention to AAH002304 represent XX
XX
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BETGETON MG, Boise
PI Picard FJ, Roy PH;
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WPI; 2001-245006/25
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Nucleic acid sequen
PT primers which can b
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The present inventi
CC mucleic acids of tuand/or primers are of acids of determined
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Sequence 23 BP; 8 A; 6 C; 4 G; 5 T; 0 other;

Gaps ö 61.0%; Score 12.2; DB 22; Length 23; 82.4%; Pred. No. 8.2e+03; tive 0; Mismatches 3; Indels 14; Conservative

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2 CATGCATGCATTACGTA 18

chagcardcarrardca 19

ABX14112 standard; DNA; 24 BP

ABX14112;

25-FEB-2003 (first entry)

Human zinc finger protein 8.8 specific RT-PCR primer, #2.

Zinc finger protein 8.8; human; RT-PCR; ss; tumour; haemopathy; human immunodeficiency virus; HIV; immunological disease; inflammation; antagonist; reverse transcription; primer.

Homo sapiens

CN1352050-A.

05-JUN-2002

02-NOV-2000; 2000CN-0127133 ABSULT 15
ABX14.7
AC ABX14.7
AC ABX14.7
AX A

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The present invention discloses a novel human zinc finger protein 8.8, polynuclectide coding for the polypeptide and method for producing this polypeptide by using DNA recombination technology. The invention also discloses the method for curing several diseases, such as malignant tumour, haemopathy, human immunodeficiency virus (HIV) infection, polypeptide. The invention also discloses and various inflammations by using the polypeptide and its therapeutic action and also discloses the spapication of the polymucleotide for coding this novel zinc finger protein 8.8. The sequence presented is the reverse transcription (RT) PCR primer, #2, which was used to isolate human zinc finger protein
                                                                                                                                                           New polypeptide-human zinc finger protein 8.8 and polynucleotide for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.0%; Score 12.2; DB 24; Length 24; 82.4%; Pred. No. 8.2e+03; Live 0; Mismatches 3; Indels (
                                                                                                                                                                                                                      Example 2; Page 16 (disclosure); 32pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 24 BP; 5 A; 5 C; 9 G; 5 T; 0 other;
                                       (BODE-) BODE GENE DEV CO LTD SHANGHAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GCATGCATGCATTACGT 17
02-NOV-2000; 2000CN-0127133.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCTGCATGCATGACCT
                                                                                                                                                                                encoding such polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                     WPI; 2002-644445/70
                                                                               Mao Y, Xie Y;
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Gaps

completed: December 31, 2003, 15:08:16 ne : 578.975 secs

Search co

Murphy KM,

Rice RN,

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veterinary; gene therapy; electromobility shift assay; EMSA; Oct-factor protein; N-Oct-1; N-Oct-3; probe; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oct-dpm8, probe used for EMSA of Oct-factor proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 23 BP; 8 A; 5 C; 5 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match

Best Local Similarity

Best Local Similarity

Matches 14; Conservative 0;

Matches 14; Conservative 0;

Matches 14; Conservative 0;

Decorporation of the conservative of the
                                                                                                                   Graham MW,
EXEXERETEXEXERS CONTROL OF THE CONTR
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Gaps

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Indels

Length 23;

Score 12.2; DB 22; Pred. No. 8.2e+03;

0; Mismatches

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The invention relates to a method of inducing, promoting or otherwise facilitating a change in the phenotype of an animal cell or group of animal cells. The modulation of phenotypic expression is conveniently accomplished via genotypic manipulation through such means as reducing translation of transcript to proteinaceous product. The ability to induce, promote or otherwise facilitate the silencing of expressible genetic sequences provides a means for modulating the phenotype in, for example, the medical, veterinary and the animal husbandry inclustries. Genetic construct comprising nucleotide sequence substantially identical to target endogenous sequence of nucleotides is in the genome of a vertebrate animal cell, is useful for altering the phenotype of a vertebrate animal cell, where the phenotype is conferred or otherwise facilitated by the expression of an endogenous conferred or otherwise facilitated by the expression of an endogenous conferred or otherwise facilitated by the expression of an endogenous in gene therapy in a vertebrate animal (e.g. human, primate, livestock animal, laboratory test animal or a murine species, avian species, fish or reptile. The present sequence is a double-stranded DNA probe used for a lectromobility shift assay (EMSA) of Oct-factor proteins, N-Oct-1 and N-Oct-3. This sequence is used in the co-suppression of Brn-2 transcription factor, which belongs to a class of Oct-factors; in MM95L
                                                                                                                                                                                                                                                                                Genetic construct for generating transgenic animal cells and in gene therapy of vertebrate animal, comprises nucleotide sequence identical to endogenous target sequence in the genome of vertebrate animal cell
         (QUEE-) STATE QUEENSLAND DEPT PRIMARY IND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 19; Page 114; 176pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         melanoma cells in vitro,
                                                                                                                                                                                       WPI; 2001-596939/67
                                                                                                  Graham MW,
         The invention relates to a method of inducing, promoting or otherwise facilitating a change in the phenotype of an animal cells or group of animal cells. The modulation of phenotypic expression is conveniently carcomplished via genotypic manipulation through such means as reducing translation of transcript to proteinaceous product. The ability to induce, promote or otherwise facilitate the silencing of expressible genetic sequences provides a means for modulating the phenotype in, for example, the medical, veterinary and the animal husbandry industries. Genetic construct comprising nucleotide sequence substantially identical to target endogenous sequence of nucleotides in the genome of a vertebrate animal cell, where the phenotype is conferred or otherwise facilitated by the expression of an endogenous the phenotype of a vertebrate animal cell, where the phenotype is conferred or otherwise facilitated by the expression of an endogenous of gene, and also in the generation of animal (e-glis, luman, primate, livestock animal, laboratory test animal or a murine species, avian species, fish or reptile. The present sequence is a double-stranded DNA probe derived from simian virus 40 (SV40) enhancer sequence and is used for electromobility shift assay (EMSA) of oct-factor proteins, N-Oct-1 and N-Oct-3. This sequence is a used in the co-suppression of Energy i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-Oct-3. This sequence is used in the co-suppression of Brn-2 transcription factor, which belongs to a class of Oct-factors, in MM96L
                                                                                                                                                                                                                                                                       Genetic construct for generating transgenic animal cells and in gene therapy of vertebrate animal, comprises nucleotide sequence identical to endogenous target sequence in the genome of vertebrate animal cell
(QUEE-) STATE QUEENSLAND DEPT PRIMARY IND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 19; Page 114; 176pp; English.
                                                                                             Murphy KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               melanoma cells in vitro.
                                                                                         Rice RN,
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S. pneumoniae phpla gene detection nucleotide sequence SEQ ID NO:2026
                                                         Gaps
                                                                                                                                                                                                                                                                                                    Species specific, genus specific, family specific, probe, detection, identification, algal, archaeal, bacterial; fungal; parasitical; microorganism, diagnosis, translation elongation factor Turnslation elongation factor G; RecA recombinase, resistance, catalytic subunit of proton-translocating ATPase; antimicrobial;
                                                         ö
                         61.0%; Score 12.2; DB 22; Length 23; 82.4%; Pred. No. 8.2e+03; ive 0; Mismatches 3; Indels (
Sequence 23 BP; 9 A; 4 C; 6 G; 4 T; 0 other;
                                                                                    19
                                                                                                                                                                                       BP.
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19-MAY-2000; 2000CA-2307010.
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                                                                                   3 ATGCATGCATTACGTAC
                                                                                                                                                                                       AAH02033 standard; DNA; 23
                                                                                                                                                                                                                                               (first entry)
                                     Local Similarity 82.4
                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                vaccine; primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200123604-A2
                                                                                                                                                                                                                                               24-JUL-2001
                                                                                                                                                                                                                  AAH02033;
                            Query Match
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AAD45370 standard; DNA; 20

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated human DNA repair polypeptide useful for diagnosing, preventing or treating cancer, or for in vitro purposes related to scientific research, synthesis of DNA and manufacture of DNA vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                          therapeutic; cancer; therapy; immunogen;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lung cancer; prostate cancer; ovarian cancer; breast cancer;
colon cancer; stomach cancer; DNA replication error;
genetic recombination error; hereditary susceptibility to cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Ruben SM, Wei Y, Adams MD, Fleischmann RD; Fuldner RA, Kirkness EF, Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; DNA repair protein; HMLH1; human mut L homologue 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human mut L homologue 1 (HMLH1) sequencing primer #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytostatic; gene therapy; sequencing; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 BP; 7 A; 4 C; 5 G; 4 T; 0 other;
                                                                                                                                                                                            Human MLH1 cDNA amplifying PCR primer, 5283
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94US-0210143.
94US-0294312.
95WO-US01035.
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                                                                                                                                                                                                                                                          Human; DNA repair protein;
                                                                                                                                                                                                                                                                                       MLH1 protein; PCR; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-MAY-2003 (first entry)
                                                                                                                              27-DEC-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-AUG-1994;
25-JAN-1995;
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16-MAR-1994;
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AMD45370 s
AXX
AMD45370;
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AMD45370;
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Human MLH1
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Human, DNA
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Homo sapie
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Homo sapie
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The invention describes an isolated polynucleotide encoding a human DNA repair protein, which is designated human mut L homologue 1 (HMLH1). The DNA repair polynucleotide is useful for diagnostic or therapeutic purposes. The polynucleotide may be used in diagnosing or treating cancer, e.g. lung cancer, prostate cancer, ovarian cancer, breast cancer, colon cancer or stomach cancer. The DNA repair polynucleotide is particularly useful for correcting errors made during DNA replication and particularly useful for diagnosing a hereditary susceptibility to cancer. This sequence represents a primer used to sequence a region of the DNA repair protein human mut L homologue 1 (HMLH1) gene in order to
                                                                                                                                                                                                                                        New human DNA mismatch repair polynucleotides and proteins, useful for diagnosing or treating cancers (e.g. lung, prostate, ovarian or breast cancer), or for correcting errors made during DNA replication and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gape
                                                                                                                                                                   Kirkness EF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetic silencing; medical industry; animal husbandry; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 12.2; DB 25; Length 21; Pred. No. 8.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oct-WT, SV40 probe used for EMSA of Oct-factor proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             veterinary; gene therapy; electromobility shift assay; Oct-factor protein; N-Oct-1; N-Oct-3; simian virus 40;
                                                                                                                                                                   Fuldner RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 21 BP; 8 A; 4 C; 5 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                  Fraser CM, Fu
ben S, Wei Y;
                                                                                                                                                                                                                                                                                                                      Disclosure; Column 11-12; 28pp; English.
                                                                                                                                                                                Ruben S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 ATGCATGCATTACGTAC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detect mutations in the gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.0%;
82.4%;
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                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-MAR-2000; 2000AU-0006363.
24-JAN-2001; 2001AU-0002700.
                                                                          94US-0187757.
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                                                                                                       94US-0187757.
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ID AAD21015 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 ATGCCTGCATTGTGTAC
                                                                                                                                                                   Fleischmann RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                Haseltine WA, Rosen CA,
                                                                                                                                                                                                                                                                                           genetic recombination
                                                                                                                                                                                                             WPI; 2003-298135/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200170949-A1
               US6482606-B1
                                                                                                       27-JAN-1994;
                                                                          27-JAN-1994;
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                                            19-NOV-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-SEP-2001
                                                                                                                                                                   Adams MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD21015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Sequence 27 BP; 8 A; 10 C; 4 G; 5 T; 0 other;

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AAA74107;
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                                                                                                                                                                                                                                                                                                                                                                                                       (ECHT/)
(NELS/)
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Matches
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                                                                                                                        RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR primers AAA15193-94 were used to amplify DNA downstream of tatA. The specification describes describes virulence proteins which are encoded by an operon including tatA, tatB, tatB, tatB, mdoG, creC, recG, yggN, eckl, irob, iroC, irob, mtd2 or ms1-16 genes obtained from Escherichia coli K1. The virulence proteins and polynucleotides, and their vaccines are useful for screening potential drugs, for the detection of virulence, and for treating or preventing conditions associated with infection by a Gram negative bacterium particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide encoded by an operon including genes from Escherichia coli for screening potential drugs, detecting virulence and treating conditions associated with infection by a Gram negative bacterium -
Probe #2 (AAQ46967) hybridises to, and is specific for, the 16S rRNA S.pyogenes. Hybridisation was enhanced by the use of "helper probes" AAQ46911 and AAQ46971. The probe can be used alone or in a mix with other S.pyogenes-specific probes to distinguish S.pyogenes from closely related bacteria (i.e. other Streptococcus spp.).
                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shea JE;
                                                                                                                                                                                                                                                                                           Virulence protein, tatA, tatB, tatC, tatE, mdoG, creC, recG, yggN, eckl; iroD, iroC, iroE, mtd2, ms1, vaccine, infection; Gram negative bacterium; PCR primer; ss.
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                                                                                       63.0%; Score 12.6; DB 14; Length 26; 78.9%; Pred. No. 5.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Holden DW,
                                                                                                            4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dougan G,
                                                                 Seguence 26 BP; 5 A; 8 C; 6 G; 7 T; 0 other;
                                                                                                            Mismatches
                                                                                                                                                                                                                                                                        PCR primer for DNA downstream of tatA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Everest PH,
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                                                                                                                                2 CATGCATGCATTACGTACG 20
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98GB-0024570.
98GB-0027814.
98GB-0027815.
98GB-0027816.
99GB-000708.
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                                                                                                                                                                                                                                                   (first entry)
                                                                                                           15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MICR-) MICROSCIENCE LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clarke EE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-376550/32.
                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                       Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                            WO200028038-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-JAN-1999;
13-JAN-1999;
28-JAN-1999;
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17-DEC-1998;
13-JAN-1999;
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Feldman RG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to loblolly pine polynucleotides with one or more Simple Sequence Repeats (SSRs) (see AAA74026-A4322). SSRs are also known as microsatellite DNA repeats. The SSRs are useful as genetic markers for genetic mapping, population genetics studies and inheritance studies in various plant breeding programmes. The present sequence is a PCR primer used for detecting the presence of a SSR locus in a pine genomic DNA sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polynucleotide having simple sequence repeat useful as markers in plants for genetic characterization e.g. genetic mapping study, an inheritance study of a commercially important trait in a plant breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               microsatellite DNA repeat; genetic marker; mapping; inheritance study; population genetics study; plant breeding programme; ss.
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                          Length 27;
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                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCR primer; loblolly pine; Simple Sequence Repeat; SSR;
                                                                                                                                                                                                                                                                                                                                                                                                                        Forward PCR primer for loblolly pine locus RIPPT658.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.0%; Score 12.2; DB 21;
82.4%; Pred. No. 8.1e+03;
ive 0; Mismatches 3;
                        Score 12.6; DB 21;
Pred. No. 5.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 BP; 7 A; 4 C; 3 G; 6 T; 0 other;
                                                                      0; Mismatches
                                                                                                                    2 CATGCATGCATTACGTACG 20
                                                                                                                                                                1 cargcarccacrcarare 19
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                                                                                                                                                                                                                                                                                     BP
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                        63.0%;
78.9%;
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                                                                      Conservative
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les 14; Conservative
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NELSON C D.
US SEC OF AGRIC.
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (INTO ) INT PAPER CO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-482836/42
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19-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                            29-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pinus taeda.
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S'.RY-CpG-RY-3'. The central CpG motifies unmethylated, and the coligonucleotides optionally have phosphorothioate linkages which make them were resistent to degradation. The invention also relates to an oligonucleotide delivery comprising an oligonucleotide of the invention and a targetting agent, and a pharmaceutical composition comprising the oligonucleotide delivery complex. The oligonucleotides are able to induce either a cell-mediated (T-cell) response or a humoral (B-cell, antibody) response, with oligonucleotides of the sequence of the sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           solid tumour cancer. The induction of an immune response is used in antisense therspy and to improve the efficacy of a vaccine. The oligonucleotide is preferably administered to lymphocytes ax vivo, producing activated lymphocytes which are then administered to the host.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents an immunogenic CpG oligodeoxynucleotide of the invention.
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            one of the generic sequences 5'-NNNT-CpG-WNNN-3' or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17 BP; 8 A; 3 C; 3 G; 3 T; 0 other;
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01-SEP-2000; 2000US-229307P.
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cc and comprice of S'-RY-Coc-
cc oligonucle cc them more comprising of the seq cc are able to cc of the seq cc of 
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Vaccine for immunising patient against respiratory syncytial virus, has epitopes of Paramyxoviridae P protein, and cytosine followed by guanine linked by phosphate bond-oligodideoxynucleotides
                                                                                                                                                                                                             The invention describes a vaccine comprising one or more epitopes of a Paramyxoviridae F protein, and one or more CpG (cytosine followed by guanine linked by phosphate bond)-oligodideoxynucleotides (ODNS). The vaccine is useful for vaccinating a patient especially against viruses of the Paramyxoviridae family e.g. reepiratory syncytial virus (RSV), the primary cause of viral bronchiolitis and pneumonia in infants and children, and infectious pulmonary disease in infants. RSV has been particularly implicated in death of infants that are premature, have bronchopulmonary displasia, or congenital heart conditions. This sequence represents an oligodideoxynucleotide that can be used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               group A beta-haemolytic Streptococcus; S.pyogenes; ribosomal RNA; respiratory tract infection; sinusitis; pharyngitis; meningitis; tonsillitis; septicaemia; pyoderma; endocarditis; impetigo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleotide polymers used as probes for detection of
Streptococcus pyogenes - capable of distinguishing it from
related species when used alone or as a mix
                                                                                                                                                                                                                                                                                                                                                                                                                                                       65.0%; Score 13; DB 24; Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helper Probe #7 to detect Streptococcus pyogenes rRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Pred. No. 3.1e+03; ive 0; Mismatches 0;
               (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17 BP; 8 A; 3 C; 3 G; 3 T; 0 other;
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                                                 Klinman DM;
                                                                                                                                                                                    Claim 4; Page 9; 30pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                       creation of the vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GEPR-) GEN PROBE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1993-257892/32.
                                                 Prince G,
                                                                                WPI; 2002-227118/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      helper probe; ss
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                                                 Mond JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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(USSH ) US DEPT HEALTH & HUMAN SERVICES. 26-SEP-2001 (first entry) Synthetic. AAS09645; COLUMN WEST COLUMN \*8888888888

Primers DK15 (AAT29050) and DK16 (AAT29051) were used for the PCR amplification of the ribosome binding site and signal peptide coding regions of the Bacillus stearothermophilus maltogenic alpha-amylase gene in pDN520. The PCR product was used to construct pPPFI, which also carried a gene (AAT29043) for Oerskovia xanthineolytica beta-1,3-glucanase (AAR97362). Transformation of Bacillus subtilis strain DN1885 or protease-deficient strain 70046 allowed prodn. of the Oerskovia lytic enzyme.

Sequence 28 BP; 10 A; 5 C; 8 G; 5 T; 0 other;

Gaps ö 68.0%; Score 13.6; DB 17; Length 28; 80.0%; Pred. No. 1.6e+03; ive 0; Mismatches 4; Indels Query Match
Best Local Similarity 80.0
Matches 16; Conservative

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MASO9645 standard; DNA; 17 BP.

Immunoreactive CpG sequence-containing oligonucleotide #95.

IfN-gamma; humoral; antibody production; interleukin-6 production; therapeutic; allergy; asthma; cancer; autoimmune disorder; infection; bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis; coryza; hay fever; urticaria; hives; food allergy; atopic condition; hepatitis; human immunodeficiency virus; HIV; malaria; Francisella; lupus erythematosus; rheumatoid arthritis; multiple sclerosis; schistcosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS; Leishmania; Ebola; Anthrax; Listeria; ss. sequence; immune response; non-B cell activation; interferon

WO200151500-A1.

19-JUL-2001.

12-JAN-2001; 2001WO-US01122

14-JAN-2000; 2000US-0176115

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Verthelyi Ishii K, Klinman D,

WPI; 2001-442129/47.

Oligodeoxynucleotides for inducing an immune response to treat and prevent an allergic reaction, cancer, an autoimmune disorder and symptoms resulting from exposure to bio-warfare agents, comprise Claim 5; Page 43; 48pp; English. multiple CpG sequences

nucleotides comprising multiple CpG sequences, where one of the CpG sequences is different from another of the multiple CpG sequences. The ODN are useful for inducing an immune response, preferably a cell-mediated immune response, involving non-B cell activation, interferon gamma (IRN-gamma) production or a humoral immune response involving B cell activation, antibody and interleukin-6 production in a host, for treating, preventing or ameliorating an allergic reaction, e.g. asthmacancer, e.g. solid tumour cancer, a disease associated with the immune AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10

or a symptom resulting from exposure to bio-warfare agent in a human. The induction of immune response improves the efficacy of a vaccine and is used in antisense therapy. The ODN are useful for treating, preventing or ameliorating allergic reactions, including eczema, allergic rhinitis or coryza, hay fever, bronchial asthma, urticaria (hivès), food allergies and other atopic conditions, for improving the efficacy of vaccines against hepatitis A, B and C, human immunodeficiency virus (HIV) and malaria, for treating immune system deficiencies, e.g. lupus erythematosus and autoimmune diseases such as rheumatoid arthritis and multiple sclerosis, infections including Francisella, schistosomiasis, tuberculosis, acquired immunoselficiency syndrome (AIDS), Leishmania and symptoms resulting from exposure of bio-warfare agent, including Ebola, system e.g. autoimmune disorder or an immune system deficiency, infection Anthrax and Listeria. 

Sequence 17 BP; 8 A; 3 C; 3 G; 3 T; 0 other;

Gaps . 0 Length 17; 0; Indels DB 22; L 3.1e+03; 65.0%; Scor. 100.0%; Pred. No. 3... 0; Mismatches Query Match 65.0 Best Local Similarity 100. Matches 13; Congervative

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RESULT 5

AAC80675/c ID AAC80675 standard; DNA; 17 AAC80675;

BP.

14-FEB-2001 (first entry)

Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:95.

CpG oligodeoxynucleotide, unmethylated; antigen-presenting cell; immunogenic; cytokine release; natural killer cell; NK cell activation; cell-mediated immune response; T-cell response; humoral response; cell-mediated immune response; memora response; buccine; allergy; asthma; infection; immune response induction; vaccine; allergy; asthma; infection; bacterial; viral; fungal; protozoal; parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus; rheumatoid arthritis; multiple sclerosis; solid tumour; cancer; immune deficiency; biological warfare agent; cytostatic; antiarthritic; antimicrobial; antiallergic; protozoacide; tuberculostatic; antiarthritic; antiathmatic; dermatological; phosphorothioate; ss. 

Synthetic.

WO200061151-A2.

19-OCT-2000.

12-APR-2000; 2000WO-US09839.

12-APR-1999; 99US-0128898

KLIN/) KLINMAN D. SHII K. ISHI

(VERT/) VERTHELYI D.

Verthelyi D; Klinman D, Ishii K,

WPI; 2001-006880/01.

Novel oligonucleotides useful for the prevention and treatment of allergies, cancer, and autoimmune disorders and for ameliorating symptoms resulting from exposure to a bio-warfare agent

Claim 4; Page 38; 46pp; English.

The invention relates to novel immunogenic CpG oligodeoxynucleotides (AAC80581-C80723). The oligonucleotide are at least 10 bases long

cell and reducing

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Gaps

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Length 20;

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anti-inflammatory; dermatological; ophthalmological; anti-psoriatic; manusouppressive; DNA repair; proliferation inhibitor; apoptosis; tumour necrosis factor inhibitor; photoaging; hyperproliferative disease; carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
                                                                                                                                                  AAZ10692-97 represent DNA fragments that are used for increasing p53 activity in a cell. The oligonucleotides are are UV minetics and protect cells against subsequent exposure to UV-irradiation or chemicals. The oligonucleotides are useful for increasing p53 activity in a cell, reducing the susceptibility to UV-induced hyperproliferative diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        melanogenic; oligomer; cytostatic; anti-allergic; p53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 20; DB 20; Length 2
100.0%; Pred. No. 0.83;
... n. Mismatches 0; Indels
DNA fragments useful for increasing p53 activity in a cel
susceptibility to UV-induced hyperproliferative diseases
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                                                                                                                                                                                                                                                                                                                                                                            and reducing susceptibility to skin cancer.
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                                                                                              Claim 11; Page 30; 44pp; English
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modified_base
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anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and immunosuppressive activities, function as 'ultra-violet mimics' to induce DNA repair processes (or a protective response to later exposure to radiation or chemicals), as a proliferation inhibitor, apoptosis inducer or a tumour necrosis factor inhibitor. Probably they mimic products of DNA damage, or processed DNA-damage intermediates, by inducing the p53 pathway, resulting in transient arrest of cell growth, allowing more time for DNA repair to occur before cell division takes place. The method is capecially used to treat cardinoma but may also be used to: treat other hyperproliferative states (e.g. psoriasis or precancerous conditions); reduce photoaging, oxidative stress or damage; prevent skin cancer; treat allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in cells caused by radiation or chemicals; increase melanin production (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to (pigmentation) in epithelial cells that contain damaged DNA. Also coligomucleotides that contain non-hydrolyzable backbones are used to inhibit apoptosis, in response to DNA damage, in epithelial cell This esquence is melanogenesis associated oligomucleotide #8, a synthetic of Thymine dimers and one of the oligomucleotides used to inhibit mammalian cell the intention.
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Matches 20; Conservative
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ABA99666
ABA99666
ABI88044
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AAQ24823
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AAV93571
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cancer; ss
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                        December 31, 2003, 11:36:21; Search time 577.975 Seconds (without alignments) 93.410 Million cell updates/sec
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4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*

5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*

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13: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*

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| SIDS1/gcgdata/geneseq_geneseq_n-embl/NA1997.DAT:+
| SIDS1/gcgdata/geneseq_geneseq_n-embl/NA1999.DAT:+
| SIDS1/gcgdata/geneseq_geneseq_n-embl/NA1999.DAT:+
| SIDS1/gcgdata/geneseq_geneseq_n-embl/NA2090.DAT:+
| SIDS1/gcgdata/geneseq_geneseq_n-embl/NA2000.DAT:+
| SIDS1/gcgdata/geneseq_geneseq_n-embl/NA2001A.DAT:+
| SIDS1/gcgdata/geneseq_geneseq_n-embl/NA2001A.DAT:+
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| SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.
| SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.
| SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.
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Compugen Ltd.
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Minimum DB seq length: 0

Maximum DB seq length: 30

Spot-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries
                 GenCore version (c) 1993 - 2003
                                                                                    nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Perfect score:
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OX40 reverse PCR p Human monoclonal a Capture oligonucle Capture oligonucle Primer EBA-D. Syn Oligonucleotide SE Oligonucleotide SE Human B-raf substr Vector pZL1 revers

Green filamentous S. pneumoniae pbpl NAAT related fluor Oligonucleotide ad 2-methyl-epothilon Yeast cystathionin Human papillomavir

Oligonucleotide ad Oligonucleotide ad Oligonucleotide ad Oligonucleotide #1

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S. pneumoniae pbpl Human zinc finger

Oct-dpm8, probe

Human MLH1 cDNA am Human mut L homolo Oct-WT, SV40 probe

Forward PCR primer

ALIGNMENTS

Rhodobacter sphaer Rhodobacter sphaer Rhodobacter sphaer

E7 mRNA PCR primer

Rhodobacter

PCR primer used to Primer derived fro

p53 activity, UV mimetic, UV-irradiation, UV-induced dermatosis, UV-induced hyperproliferative disease, psoriasis, vitiligo, atopic dermatitis, allergic rhinitis, conjunctivitis, photoaging, Oligonucleotide sequence that increases p53 activity in a cell Eller M; 99GB-0006758 98US-0048927 Gilchrest BA, Yaar M, BOSTON (UYBO-) UNIV 24-MAR-1999; 26-MAR-1998; GB2336157-A. 13-0CT-1999. Synthetic. 

WPI; 1999-543520/46

Immunocactive CpG Immunogenic CpG ol Immunostimulatory Helper Probe #7 to PCR primer for DNA

AAZ10697 AAS14912 AAT29051 AAS09645 AAC80675 ABK46523 AAQ46972 AAA15194

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Melanogenesis asso Maltogenic alpha-a Oligonucleotide se

**Description** 

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Query Match Length

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Result ŝ

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PAT 15-MAY-2001
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 15)
Choudhary,G., Hahnenberger,K., Kuekes,P.J., Lichtenwalter,K. and Harnock,W.B.
Method of binding a plurality of chemicals on a substrate by electrophoretic self-assembly
Patent: US 6107038-A 1 22-AUG-2000,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brennan, T.M., Chatelain, F. and Berninger, M.
Method and apparatus for performing large numbers of reactions
using array assembly
Patent: WO 21397-A 2 19-APR-2001,
Protogene Laboratories, Inc. (US)
Location/Qualifiers
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Sequence 2 from Patent WO0127327.
AX133943
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/organism="Homo sapiens"
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Search completed: December 31, 2003, 17:09:50 Job time : 1844.27 secs

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PAT 20-DEC-2002
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Unclassified.
1 (bases 1 to 15)
Choudhary.G., Hahnenberger,K., Kuekes,P.J., Lichtenwalter,K. and Hancock,W.S.
Method of binding a plurality of chemicals on a substrate by electrophoretic self-assembly Patent: US 6107038-A 1 22-AUG-2000;
Location/Qualifiers
                                                                                                                                                                                                                                                   1 (bases 1 to 30)
Brzostowicz, P.C. and Rouviere, P.B.
Brzostowicz, P.C. and Rouviere, P.B.
Oxidation of a cyclohexanone derivative using a Brevibacterium cyclohexanone monooxygenase
cyclohexanone monooxygenase
Patent: US 6465224-A 43 15-OCT-2002;
Location/Qualifiers
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100.0%; Pred. No. 2.2e+05;
ive 0; Mismatches 0;
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82.4%; Pred. No. 1.6e+05;
iive 0; Mismatches 3;
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                                                                               AR236687 30 bp 1 Sequence 43 from patent US 6465224.
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Sequence 1 from patent US 6107038.
AR106386
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Unclassified.
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AR236687
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Unclassified.
1 (bases 1 to 30)
Brzostowicz, P.C. and Rouviere, P.E.
Genes and enzymes for the production of adipic acid intermediates
Genet uS 636376-A 43 02-APR-2002;
Patent: US 6365376-A 43 02-APR-2002;
Location/Qualifiers
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                                                                                   Length 23;
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Pred. No. 1.6e+05;
0; Mismatches 3;
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Pred. No. 1.6e+05;

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|mol type="genomic DNA"
    db_xref="taxon:32630"

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Patent: WO 0216649-A 2034 28-FEB-2002;
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Sequence 2034 from Patent WO0216649.
AX445579
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Sequence 43 from patent US 6365376.
AR203427
AR203427.1 GI:21499813
/note="Oligonucleotide"
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Location/Qualifiers
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Best Local Similarity 82.4%;
Matches 14; Conservative
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AX111293.1 GI:13927585
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Matches 14; Conservative
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JP 200232588-A/18.
synthetic construct
artificial sequences.
1 (bases I to 20)
Fraser.C.M., Ruben,S.M., Wei,Y.F., Adams,M.D., Fleischmann,R.D.,
Human DNA mismatch repair proteins
Patent: JP 2002325588-A 18 12-NOV-2002;
HUMAN GENOME SCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAT 15-MAY-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRAIG A ROSEN
CI2N15/09, C07K14/47, C12P21/02, C12Q1/68//(C12P21/02, C12R1:19),
C12N15/00
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Haseltine, W.A., Ruben, S.M., Wei, Y.-F., Adams, M.D.,
Fleischmann, R.D., Fraser, C.M., Fuldner, R.A., Kirkness, E.F. and
Rosen, C.A.
Human DNA mismatch repair proteins
Patent: US 6416984-A 21 09-JUL-2002;
Location/Qualifiers
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                                                                                                                                                                      65.0%; Score 13; DB 6; Length 17; 100.0%; Pred. No. 6.1e+04; ive 0; Mismatches 0; Indels
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PR 27-JAN-1994 US 08/187757,16-MAR-1994 US
23-AUG-1994 US 08/294312
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"
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Sequence 21 from patent US 6416984.
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JP 2002325588-A/18
12-NOV-2002
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Bergeron, M.G., Boissinot, M., Huletsky, A., m Nard, C., Ouellette, M., Picard, F.J. and Roy, P.H.
Highly conserved genes and their use to generate probes and primers for detection of microorganisms
Patent: WO 0123604-A 2026 05-APR-2001;
Infectio Diagnostic (I.D.I.) INC. (CA)
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Adams, M.D., Fleischmann, R.D., Fraser, C.M., Fuldner, R.A.,
Kirkness, E.F., Haseltine, W.A., Rosen, C.A., Ruben, S. and Wei, Y.-F.
Human DNA mismatch repair polynucleotides
Patent: US 6482606-A 19 19-NOV-2002;
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/organism='Artificial Sequence'.
Location/Qualifiers
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Pred. No. 1.7e+05;
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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/organism="synthetic construct"
/mol type="genomic DNA"
/db_xref="taxon:32630"
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Sequence 2026 from Patent WO0123604.
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AR255705
AR255705.1 GI:27304802
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Gaps

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PAT 28-AUG-2001

FEATURES

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1 (bases 1 to 28)
Mori,M., Okuno,T. and Furusawa,I.
Process for production of exogenous gene or its product in plant
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Oligodeoxymucleotide and its use to induce an immune response
Patent: WO 0151500-A 95 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)
Location/Qualifiers
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Vaccine against RSV
Patent: WO 0211761-A 113 14-FEB-2002;
HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
                                                                                                                                                                                                                                                   Length 28;
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Pred. No. 3.5e+04;
0; Mismatches 1;
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/mol type="genomic DNA"
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    .17
    /organism="synthetic construct"
/mol_type="genomic DNA"

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                                                                                      Patent: US 5418153-A 10 23-MAY-1995;
Location/Qualifiers
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AX465445
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Sequence 95 from Patent WO0151500.
AX194495
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/organism="unknown"
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Best Local Similarity 93.3
Matches 14; Conservative
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TITLE
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Artificial sequence; Genes.
JP 1994046874-A/10
22-FEB-1994
27-APR-1993 JP 1993122189
28-APR-1992 JP 92P 152599
MORI MASAYUKK, OKNO TETSUO, FURUSAWA IWAO
C12P21/02,A01H5/00,C12N5/10,C12N15/11, PC
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JP 1994046874-A/10.
Synthetic construct
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1 (bases 1 to 28)
Mori, M., Okuno, T. and Purusawa, I.
EXCRENTE IN PLANT CELL AND PRODUCTION OF ITS PRODUCT
NIPPON NOHYAKU, CO LTD
NIPPON NOHYAKU, CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.0%; Score 13.4; DB 6; Length 28; 93.3%; Pred. No. 3.5e+04; Live 0; Mismatches 1; Indels
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                1...20
/organism="synthetic construct"
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Sequence 10 from Patent US 5418153.
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strandedness: Single;
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hypothetical: No;
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PAT 16-JUL-2002

RESULT 3 I12026/c LOCUS

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                    Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Gapop 10.0 , Gapext 1.0
Searched: 2888711 seqs, 20454813386 residues

Protal number of hits satisfying chosen parameters:

Ninimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SUMMAKIES	ion	60 AX26876	E06768 Synthe	I12026 S	AX194495	AX465445	AR217681	BUIBLILA	AX111293	AX445579	AR203427	AR236687	AK105386	)	AX133943	AX683917	A83415 S0	BD133367	AR213170	AX464822 AX100899		AX446872	AX403021	AX039554	AR065159	AR136789	AR217384 123329 St	127356 Se		AR149933	AR148349	AR153693	AX213034 AX289339	AR106598	AX0///32	E06768 Sy		ALIGNMENTS		20 bp DNA linear PAT 29-OCT-2001 174342.			
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us-09-540-843-7.szlm30.rnpb

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APPLICANT: Ribozyme Pharmaceuticals Inc.

TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REPERBACE: MBHB00-801-F
CURRENT APPLICATION NUMBER: US/09/817,879
CURRENT FILING DATE: 2001-03-26
SUFTRARE: Patentin version 3.0
SUFTWARE: Patentin version 3.0
SEQ ID NO 4624
LENGTH: 13
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ORGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: Oligonucleotide NET-4 oligo 868 used for in-situ
COTHER INFORMATION: hybridization
So-09-875-440-22
                                                                                                                                                                                                                                                                                                                                                                         TYPE: RNA

TYPE: RNA

TYPE: RNA

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FRATURE:

NAME/KEY: misc_feature

LOCATION:

OTHER INFORMATION: oligonucleotide substrate

OCHEN INFORMATION: OCHEN INFORMATION: oligonucleotide substrate

OCHEN INFORMATION: OCHEN INFORMA
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Best Local Similarity 100.
Matches 7; Conservative
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Search completed: January 1, 2004, 01:10:38 Job time : 82.6076 secs

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APPLICANT: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relater TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relater TITLE OF INVENTION: Hepatitis C Virus Infection FILE REFERENCE: RPI 400/003
CURRENT APPLICATION NUMBER: US/09/740,332
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9704
SEPTAME: Patentin version 3.0
SEPTAME: Patentin version 3.0
LENGTH: 13
                     Publication No. US20030125241A1

Fublication No. US20030125241A1

GENERAL INFORMATION:

APPLICANT: WISSENBACH, MARGIT

APPLICANT: WORW, HENRICK

APPLICANT: WORW, HENRICK

APPLICANT: HANSEN, BO

TITLE OF INVENTION: THERAPEUTIC USES OF LNA-MODIFIED OLIGONUCLEOTIDES IN

TITLE OF INVENTION: THERAPEUTIC USES OF LNA-MODIFIED OLIGONUCLEOTIDES IN

TITLE OF INVENTION: THERAPEUTIC USES OF LNA-MODIFIED OLIGONUCLEOTIDES IN

TITLE OF INVENTION: THERAPEUTIC USES OF LNA-MODIFIED OLIGONUCLEOTIDES IN

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TITLE OF INVENTION: THERAPEUTIC USES OF LNA-MODIFIED OLIGONUCLEOTIDES IN

TITLE OF INVENTION: UNFERRE (5/2120)

CURRENT APPLICATION NUMBER: 60/291,830

PRIOR FILING DATE: 2001-06-18

NUMBER OF SEQ ID NOS: 16

SEQ ID NO 16

LENGTHERAPEUTIC USES OF LNA-MODIFIED OLIGONUCLEOTIDES IN

LENGTHERAPEUTIC USES OF LNA-MODIFIED OLIGONUCLEOTIDES IN

TITLE REFERENCE: 2003-02-07

STATUTE OF INVENTION: 100-02-07

PRIOR THERAPEUTIC USES OF LNA-MODIFIED OLIGONUCLEOTIDES IN

TITLE OF INVENTION: 100-02-07

TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: DNA oligonucleotide with phosphorothicate backbone
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    LOCATION:
    CTHER INFORMATION: oligonucleotide substrate
US-09-740-332-4624

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4624, Application US/09817879; Publication No. US20030171311A1; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 71.4
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Best Local Similarity 100.
Matches 7; Conservative
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11 AGTATGA 5
JS-10-150-779A-16/C
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Sequence 15, Application Us/10150779A

Publication No. US20030125241A1

GENERAL INFORMATION:

APPLICANT: WISSENBACH, WARGIT

APPLICANT: KOCH, TROELS

APPLICANT: KOCH, TROELS

APPLICANT: HANSEN, BO

TITLE OF INVENTION: THERAPEUTIC USES OF LNA-MODIFIED OLIGONUCLEOTIDES IN

TITLE OF INVENTION: THERAPEUTIC USES OF LNA-MODIFIED OLIGONUCLEOTIDES IN

TITLE OF INVENTION: THERAPEUTIC USES OF LNA-MODIFIED OLIGONUCLEOTIDES IN

TITLE OF INVENTION: THERAPEUTIC USES OF LNA-MODIFIED OLIGONUCLEOTIDES IN

TITLE OF INVENTION: UNPERE: US/10/150, 779A

CURRENT FILING DATE: 2003-02-07

PRIOR FILING DATE: 2001-05-18

NUMBER OF SEQ ID NOS: 16

SEQ ID NO 15

LENGTH: 12
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; Sequence 1423, Application US/10033145
; Publication No. US20020151515A1
; Fabricant General Corporation
; APPLICANT: GENERAL SHUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; TITLE OF INVENTION PREPARATION AND USE OF SUPERIOR VACCINES
; TILLE REFERENCE: GAOJOL CORPORATION OF STATEMENT OF ST
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Matches 7; Conservative
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CURRENT APPLICATION NUMBER OF SEQ 1D NOS: 199
RIOR APPLICATION NUMBER OF SEQ 1D NOS: 199
SOFTWARE: Patentin verification of Type: DA ORGANISM: Homo sapient Organism: Patentin verification of Type: DA ORGANISM: Homo sapient Organism: Patentin verification of Type: DA ORGANISM: Homo sapient Organism: Patentin of Type: DA ORGANISM: Homo sapient Organism: Patentin of Type: DA ORGANISM: HOMO SEGURAL 11
SEGULT 11
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US-10-329-465-30/c
US-10-329-465-30/c
US-10-329-465-30/c
Sequence 30, Application US/10329465
Fublication No. US20030165949A1
GENERAL INFORMATION:
APPLICANT: Wang et al.
TITLE OF INVENTION: GENES ABNORMALLY EXPRESSED IN MYELOID LEUKEMIA CELLS WITH AN MLL-1
TITLE OF INVENTION: FUBSION
TITLE OF INVENTION WIMBER: US/10/329,465
CURRENT APPLICATION NUMBER: US/0/343,826
FRIOR PILING DATE: 2001-12-27
NUMBER OF SEQ ID NOS: 315
SEQ ID NO 30
IENGTH: 10
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
US-09-398-399-31
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wolber, Pual K.
APPLICANT: Wolber, Pual K.
TITLE OF INVENTION: Arrays Having Background Features and
TITLE OF INVENTION: Methods for Using the Same
FILE REFERENCE: 10010760-1
CURRENT APPLICATION NUMBER: US/09/899,381
CURRENT PAPLICATION NUMBER: 09/398,399
PRIOR APPLICATION NUMBER: 09/398,399
PRIOR PILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 31
LENGTH: 10
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                                                                              100.0%; Score 7; DB 9; Length 10; 100.0%; Pred. No. 1.1e+05;
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1.1e+05;
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; OTHER INFORMATION: Synthetic oligonucleotide
US-10-329-465-30
                                                                                                                       0; Mismatches
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Patent No. US20020068293A1
GENERAL INFORMATION:
APPLICANT: Delenstarr, Glend C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: synchetic probe US-09-899-381-31
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Best Local Similarity 100...
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Matches 7; Conservative
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Matches 7; Conservative
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1 AGTATGA 7
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APPLICANT: LEFKOWITZ, STEVEN M.
APPLICANT: LUEBKE, KEVIN J.
APPLICANT: LUEBKE, KEVIN J.
APPLICANT: SAMPRAS, NICHOLAS M.
APPLICANT: MOLBER, PAUL K.
TITLE OF INVENTION: ACIDS TO SURFACES
FILE REFERENCE: 10991620-1
CURRENT PRILING DATE: 1999-09-17
SUMBER OF SEQ ID NOS: 35
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                         Gaps
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                                                                                             Query Match 100.0%; Score 7; DB 15; Length 9; Best Local Similarity 100.0%; Pred. No. 3.7e+08; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 7; DB 15; Length 9; 100.0%; Pred. No. 3.7e+08; Pred. 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Method to Inhibit Cell Growth Using TITLE OF INVENTION: Oligonucleotides File Reference: 0054.1088-019 CURRENT APPLICATION NUMBER: US/10/122,633 CURRENT FILING DATE: 2002-04-12 PRIOR APPLICATION NUMBER: US 09/540,843 PRIOR PILING DATE: 2000-03-31 PRIOR APPLICATION NUMBER: PCT/US01/10162 PRIOR FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                   ) OTHER INFORMATION: Synthetic DNA Fragment US-10-122-630-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 31, Application US/09398399
Patent No. US20020051973A1
GENERAL INFORMATION:
ORGANISM: Artificial Sequence
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C Best Local Similarity 100.0%

Matches 7; Conservative

Matches 1 AGTATGA 7
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AGTATGA 8
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AGTATGA 8
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LENGTH: 10
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                                                                                                                                                                                                                                                                 Sequence 7. Application US/10122633

Publication No. US20030032611A1

GENERAL INFORMATION:

APPLICANT: Glier, Mark S.

APPLICANT: Eller, Mark S.

APPLICANT: Yaar, Mina

TITLE OF INVENTION: Method to Inhibit Cell Growth Using

TITLE OF INVENTION: Method to Inhibit Cell Growth Using

TITLE OF INVENTION: Oligonucleotides

TITLE OF INVENTION: Oligonucleotides

TITLE OF INVENTION: UNMERR: US/10/12,633

CURRENT APPLICATION NUMBER: US/10/12,633

FRIOR PILING DATE: 2002-04-12

PRIOR APPLICATION NUMBER: PCT/US0/10162

PRIOR APPLICATION NUMBER: PCT/US0/10162

PRIOR PILING DATE: 2001-03-30

NUMBER OF EQ. ID NOS: 15

SOFTWARE: FastSEQ for Windows Version 4.0
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J GENERAL INFORMATION:

APPLICANT: Gilchrest, Barbara A.

APPLICANT: Gilchrest, Mark S.

APPLICANT: Eller, Mark S.

TITLE OF INVENTION: Oligonuclectides

TITLE OF INVENTION: Oligonuclectides

TITLE OF INVENTION: Oligonuclectides

TILE REPERENCE: 0054.1088-018

CURRENT FILING NUMBER: US/01/22,630

CURRENT FILING DATE: 195-06-06

PRIOR FILING DATE: 1995-06-03

PRIOR FILING DATE: 1996-06-03

PRIOR PLING DATE: 1998-06-03

PRIOR PLING DATE: 1998-06-03

PRIOR PLING DATE: 1998-06-03

PRIOR PLING DATE: 1998-03-26

PRIOR PLING DATE: 2000-03-31

PRIOR FILING DATE: 2010-03-30

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1-15 PARCED
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100.0%; Score 7; DB 15; Length 7; 100.0%; Pred. No. 4.8e+08;
                                             0; Indels
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100.0%; Score 7; DB 15; I
Best Local Similarity 100.0%; Pred. No. 4.8e+08;
Matches 7; Conservative 0; Mismatches n.
                                                   0; Mismatches
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US-10-122-633-7
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ORGANISM: Artificial Sequence
Query Match
Best Local Similarity 100.
Matches 7; Conservative
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CURRENT APPLICATION NUMBER: US/10/122,633
CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: US 09/540,843
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR PLING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FRAELSEQ for Windows Version 4.0
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100.0%; Pred. No. 4.8e+08;
tive 0; Mismatches 0;
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Sequence 3, Application US/10122633

Publication No. US20030032611A1

GENERAL INFORMATION:
A APPLICANT: GILChreef, Barbara A.
APPLICANT: Bilchreef, Mark S.

APPLICANT: Yaar, Mina
APPLICANT: Yaar, Mina

APPLICANT: Yaar, Mina

ONLY ON TOWN TOWN Wethord to Inhit
                                                                                                                        US-10-122-630-7; Sequence 7, Application US/10122630; Publication No. US20030032610A1; GENERAL INFORMATION: APPLICANT: Gilchreet, Mark S.; APPLICANT: Taar, Mark S.; APPLICANT: Yaar, Mina
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 7; Conserv
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Sequence 527, App Sequence 528, App Sequence 1527, App Sequence 1559, App Sequence 1570, App Sequence 30, Appl Sequence 528, App Sequence 528, App Sequence 1570, App Sequence 1570, App Sequence 1570, App Sequence 4558, App Sequence 559, App Sequence 2750, App 
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Sequence 2751, A
Sequence 2752, A
Sequence 2753, A
Sequence 2754, A
Sequence 2755, A
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US-09-504-231A-1570

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US-09-274-553D-527

US-09-274-553D-528

US-09-274-553D-1527

US-09-274-553D-1527

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US-09-272-343-1

US-09-272-343-1

US-09-274-553D-1570

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Best Local Similarity 100.0%; Pred. No. 4.8e+08;
Matches 7; Conservative 0; Mismatches 0;
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US-09-866-108-2752
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US-10-122-630-3
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Publication No. US20030032610A1
GENERAL INFORMATION:
APPLICANT: Gilchrest, Barbara A.
APPLICANT: Eller, Mark S.
APPLICANT: Yaar, Mina
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Sequence 7, Appli
Sequence 7, Appli
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Sequence 1, Appli
Sequence 31, Appl
Sequence 31, Appl
Sequence 1423, Ap
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 4624, Ap
Sequence 4624, Ap
                                                                                                                                                                                                                                                           December 31, 2003, 17:10:00 ; Search time 81.6076 Seconds (without alignments) 296.896 Million cell updates/sec
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| cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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| cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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| cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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                                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-033-145-1423
US-10-150-779A-15
US-10-150-779A-16
US-09-740-332-4624
US-09-817-879-4624
US-09-875-440-22
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Searched: 2263443 seqs, 1730637950 residues

Chrotal number of hits satisfying chosen parameters:
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US-10-122-630-7
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US-09-899-381-31
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Raximum DB seq length: 30

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Gapop 10.0 , Gapext 1.0
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OF SEQUENCE 33. Application US/09094714A

SEQUENCE 33. Application US/09094714A

OF GENERAL INFORMATION:

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                                                                                                                     Length 15;
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                                                                                                                 100.0%; Score 7; DB 2; Le
100.0%; Pred. No. 8.6e+03;
attive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 7; DB 3; Le 100.0%; Pred. No. 8.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDION ITE:
COMPUTER: IBM PS/2
SOFTWARE: WORDPERFECT 8.0
SOFTWARE: WORDPERFECT 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/094,714A
FILING DATE: June 15, 1998
CLASSIFICATION: DATA:
APPLICATION NUMBER: 08/601,269
FILING DATE: 14-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 09/401-1995
PRIOR APPLICATION DATA:
FILING DATE: 09-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 09-JUL-1993
APPLICATION DATA:
APPLICATION WHERE: 07/852,852
FILING DATE: 16-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: PAUL CARRATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 33:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                     Query Match
Best Local Similarity luv...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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TOPOLOGY: linear
single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                            ; TOPOLOGY: linear
US-08-485-133-28
                                                                                                                                                                                                                                                                                                   9 AGTATGA 15
                                                                                                                                                                                                                                          1 AGTATGA 7
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY:
US-09-094-714A-33
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12 AGTATGA 6

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Wignord State 144-144/c

| Sequence 34, Application US/09034714A
| Patent No. 6117847
| Patent No. 611784710N; | Patent No. 611784711S, | Patent No. 61178471S, | Patent No. 611788, | Patent No. 6
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GENERAL INFORMATION:

APPLICANT: Allibert, Patrice A.

APPLICANT: Crost, Philippe
APPLICANT: Mach, Bernard F.

APPLICANT: Mach, Bernard F.

APPLICANT: Madrand, Bernard F.

APPLICANT: Tiercy, Jean-Marie
TITLE OF INVENTION: SYSTEM OF PROBES ENABLING HLA-DR TYPING
TITLE OF INVENTION: TO BE PERFORMED, AND TYPING METHOD USING SAID PROBES NUMBER OF SEQUENCES: 81

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
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Pred. No. 8.6e+03;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Blam PC compatible
COMPUTER: Blam PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,133
FILING DATE: 7-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/030,143
FILING DATE: 11-MAR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: WPB 28596A
TELECOMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
TELEFAX: 703-836-2787
          US/08/585,684B
                                                                                                                                                                                                                                                                             218/078
                                     FILING DATE: January 16, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/000,951
FILING DATE: July 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 28, Application US/08485133
Patent No. 5976789
                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 218/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELERAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1315:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: OLIFF & BERRIDGE
STREET: P.O. Box 19928
CITY: Alexandria
STATE: Virginia
ZIP: 22320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Berridge, William P. REGISTRATION NUMBER: 30,02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 15 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 71.4
Matches 5; Conservative
          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
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5 AGUAUGA 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-585-684B-1315
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TO Sequence 1315, Application US/08585684B

Sequence 1315, Application US/08585684B

Sequence 1315, Application US/08585684B

Sequence 1315, Application US/08585684B

GENERAL INFORMATION:
APPLICANT: Strinchcomb, Daniel T.
APPLICANT: McSwiggen, James

ITTLE OF INVENTION: McTHOD AND REAGENT FOR THE

ITTLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE

ITTLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE

ITTLE OF INVENTION: ADDRESS:
CORRESPONDENCES: 2751

CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon
STREET: Suite 4700

STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 7; DB 2;
Pred. No. 8.6e+03;
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νε 2; Mismatches
                                        CORRESPONDENCE ADJACATION

ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: B.COTAGE
COMPUTER READABLE FORM:
MEDIUM TYPE: B.COTAGE
COMPUTER: PateSEQ Version 1.5
SOFTWARE: FateSEQ Version 1.5
SOFTWARE: FateSEQ Version 1.5
STUING DATE: January 16, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/000,951
FILING DATE: January 16, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 32,327
ATTOMEST MOMBER: 32,327
REGISTRATION NUMBER: 32,327
TELEFRANCE/DOCKET NUMBER: 218/078
TELEFRANCE/DOCKET NUMBER: 218/078
TELEFRANCE/DOCKET NUMBER: 218/078
TELEFRANCE/SOFT NUMBER: 218/078
TELEFRANCE/SOFT NUMBER: 218/078
TELEFRANCE/SOFT NUMBER: 218/078
TELEFRANCE/SOFT NUMBER: 218/078
TELEFRANCE/STRIETICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FRSESEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||:|:||
5 AGUAUGA 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION APPLICATION POLICAL APPLICATION POLICATION APPLICATION NOT POLICATION APPLICATION APPLICAT
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Sequence 4, Application US/08747121
; Pattent No. 5874200
; GENERAL INFORMATION:
APPLICANT: Murphy, Gerald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (212)7909090
(212)8698864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Modified Base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AGTATGA 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Grandgenett, Duane
TITLE OF INVENTION: An in vitro method for concerted integration of
TITLE OF INVENTION: donor DNA molecules using retroviral integrase proteins.
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Grandgenett, Duane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTHER INFORMATION: The sequence is the bottom strand of CTHER INFORMATION: M-2 US and the pGEM target of the top clone shown in CTHER INFORMATION: Figure 14 of original application. US-08-671-071B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 7; DB 1; Length 15; Best Local Similarity 71.4%; Pred. No. 8.6e+03; Matches 5; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 7; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 8.6e+03;
Matches 7; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Distette, 3.5 inch;
COMPUTER: Gateway 2000, 4DX2-66E(Intel)
OPERATING SYSTEM: IBM clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Microsoft Word CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/671,071B FILING DATE: 06/27/96 CLASSIFICATION: 435
TELECOMUNICATION INFORMATION:
TELEPHONE: (314) 962-0064
TELEPK: (314) 577-8406
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ## ADDRESSE:

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   (213) 489-1600
                           TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 32'SEQUENCE CHARACTERISTICS: LENGTH: 15 base pairs TYPE: nucleic acid STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
US-08-334-847-327
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TELEPHONE:
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APPLICANT: BOYNTON, Alton
APPLICANT: Sengal, Anil
TITLE OF INVENTION: NUCLECTIDE AND AMINO ACID
TITLE OF INVENTION: SEQUENCES OF A D2-2 GENE ASSOCIATED WITH
TITLE OF INVENTION: BRAIN TUMORS AND METHODS BASED THEREON
UNDER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 7; DB 2; Length 15; 100.0%; Pred. No. 8.6e+03;
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APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, James
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Where N is any nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                         STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: Baldwin, Geraldine F
REGISTRATION NUMBER: 31,232
REFERENCE/DOCKET NUMBER: 8511-008
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/747,121
FILING DATE: 08-NOV-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 130, Application US/08585684B Patent No. 5877021
                                                                                                                                                                                                                                                                                                                                  ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
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Gaps
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Fatent No. 5693532

GENERAL INFORMATION:
APPLICANT: Draper, Kenneth
APPLICANT: Draper, Kenneth
APPLICANT: Pawco, Pam
APPLICANT: Pawco, Pam
APPLICANT: Pawco, Pam
APPLICANT: Woolf, Tod
TITLE OF INVENTION: INHIBITING RESPIRATORY
TITLE OF INVENTION: SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 909
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.4%; Preu. ...
                         COMPUTER: DESCRIPTION COLUMNIER: DESCRIPTION SYSTEM: IBM P.C. DOS 5.0 SUFFWARE: WOOD PERFECT 5.1 CURRENT APPLICATION DATE: WOOD PERFECT 5.1 APPLICATION NUMBER: US/08/334,847 FILING DATE: NO. 5693532ember 4, 1994 PRIOR APPLICATION DATA: APPLICATION NUMBER: FILING DATE: ATTORNATION: NAME: WAZBURT INFORMATION: REGISTRATION NUMBER: 32,327 REGISTRATION NUMBER: 32,327 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION INFO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IEM Compatible
OPERATING SYSTEM: IEM P.C. DOS 5.0 SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/334,847
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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ATTORNEY/AGENT INFORMATION:
NAME: WAZDUZG, RICHARG JZ,
REGERRATON NUMBER: 32,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 71.4
Matches 5; Conservative
             storage
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STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
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US-08-334-847-24
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AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 1 OTHER INFORMATION: Where N is any nucleotide SS-08-744-905A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: McSwiggen, James
APPLICANT: Draper, Kenneth
APPLICANT: Draper, Kenneth
APPLICANT: Pavco, Pam
APPLICANT: Woolf, Tod
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: INHIBITING RESPIRATORY
TITLE OF INVENTION: SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 909
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/744,905A
FILING DATE: 08-NOV-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Baldwin, Geraldine F
REGISTRATION NUMBER: 31,232
REFERENCE/DOCKET NUMBER: 8511-009
TELECOMUNICATION INFORMATION:
TELEPHONE: (212)790909
TELEPAX: (212)869864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                 ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 24, Application US/08334847
Patent No. 5693532
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPAX: (212)869864
TELEX: (614) PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
LENGTH: nucleic acid
STRANDEDNESS: single
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J Best Local Similarity 100.09

Matches 7; Conservative

Matches 1 AGTATGA 7
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie &
     INVENTION:
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     TITLE OF
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Sequence 27, Application US/08485133
Patent No. 5976789
GENERAL INFORMATION:
APPLICANT: Allibert, Patrice A.
APPLICANT: Cros, Philippe
APPLICANT: Madchand, Bernard F.
APPLICANT: Madchand, Bernard F.
APPLICANT: Tiercy, Jean-Marie
TITLE OF INVENTION: SYSTEM OF PROBES ENABLING HLA-DR TYPING
TITLE OF INVENTION: TO BE PERFORMED, AND TYPING METHOD USING SAID PROBES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID
TITLE OF INVENTION: SEQUENCES OF C4-2, A TUMOR SUPPRESSOR GENE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BY PC compatible
COMPUTER: APETHICH Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,133
FLING DATE: 7-JUN-1995
CLASSIFICATION NUMBER: US 08/030,143
FLING DATA:
APPLICATION NUMBER: 10.0000,143
FLING DATA: 11.0000,143
FLING DATA: 11.0000,143
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                 Mismatches
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REGISTRATION NUMBER: 30,024
REPERENCE/DOCKET NUMBER: WPB
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Murphy, Gerald
APPLICANT: Boynton, Alton
APPLICANT: Sehgal, Anil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100...
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                 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 AGTATCA 14
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                                                                                             1 AGTATGA 7
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                     Matches
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Patent No. 6528268

GENERAL INFORMATION:
APPLICANT: Anderson, Maria K.
APPLICANT: Reneland, Lars G. T.
APPLICANT: Reneland, Rikard H.
APPLICANT: Reneland, Rikard H.
APPLICANT: Reneland, Rikard H.
TITLE OF INVENTION: REAGENCE: Galzeus
FILE REFERENCE: Galzeus
CURRENT APPLICATION UNMBER: US/09/922,445

CURRENT FILING DATE: 2001-08-03

NUMBER OF SEQ ID NOS: 51

SOOTWARE: PatentIn version 3.1

LENGTH: 13
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Pred. No. 8.6e+03;
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100.0%; Pred. No. 8.6e+03;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 7; DB 3; Length 9; 100.0%; Pred. No. 4.6e+07; vative 0; Mismatches 0; Indels
EARLIER FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 9
                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: DNA Fragment US-09-048-927-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 100.
WH Best Local Similarity 100.
Matches 7; Conservative
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CORGANISM: Bynthetic
US-09-922-445-22
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Best Local Similarity
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BS-09-922-445-22
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8, Appli
55, Appl
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                                                                                                                                815,
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Sequence
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5.9e+07;
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APPLICANT: Gilchrest, Barbara A.
APPLICANT: Gilchrest, Mana
APPLICANT: Biler, Mana
APPLICANT: Biler, Mark
TILLE OF INVENTION: Use of Locally Applied DNA Fragments
TILE REFERENCE: BUS-689-68,927
CURRENT FILING DATE: 1998-03-26
EARLIER APPLICATION NUMBER: 08/952,697
EARLIER FILING DATE: 1996-06-03
EARLIER FILING DATE: 1996-06-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Fragments
                                      US-08-758-306-369
US-08-758-306-369
US-08-758-306-371
US-08-758-306-813
US-08-758-306-815
                                                                                                                                              US-08-671-320-6
US-08-68-577-6
US-08-88-133-2
US-08-985-162-443
US-08-985-162-444
US-09-207-914-6
US-07-688-352C-8
                                                                                                                                                                                                                                                                                                     US-08-363-585-55
US-08-358-995-10
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APPLICANT: Gilchrest, Barbara A.
APPLICANT: Gilchrest, Barbara A.
APPLICANT: Yaar, Mina
APPLICANT: Blier, Mark
TITLE OF INVENTION: Use of Locally Applied DNA
FILE REFERENCE: BU94-68A2
CURRENT FILING DATE: 1998-03-26
EARLIER APPLICATION NUMBER: 08/952,697
EARLIER FILING DATE: 1996-06-03
EARLIER FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FILING DATE: 1995-06-06
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Pred. No. 5.9e
; Mismatches
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Patent No. 6147056
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Patent No. 6147056
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; OTHER INFORMATION: DNA Fragment
US-09-048-927-3
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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-08-585-684B-1315
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-08-932-140C-6
-08-932-140C-7
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                                                                                                   nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Match Length
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5

E., SLC,

from the Jackson

us-09-540-843-7.szlm30.rst

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pubmoly [4] 4732114 [$pl.AR129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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|ab host="E. Coli strain XL10-Gold, Tl-resistant, F-'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone lib="Mouse 10kb plasmid UUGCiM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jack
                                                                                   Biomedical Polymers Research Bldg., 20 S. 2030
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100.0%; Pred. No. 2.4e+05;
tive 0; Mismatches 0;
                                                                                                                                                                                             Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0080 row: C column: 06
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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University of Utah Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
/clone="UUGC1M0080C06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 26.
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                                                                                                                        84112, USA
Tel: 801 585 5606
                                         University of
Rm. 308, Biome
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                                                                                                                                                                                                           Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

[ bases 1 to 25]
Alonso,J.W., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
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/clone="shuk 01564.41.95.x"
/clone="lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Lanam, L., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
J., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Welse, R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated intron of At3g22930.
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Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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    .25
    /organism="Arabidopsis thaliana"

                                                                                                                                                                           Arabidopsis thaliana (thale cress)
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/strain="Columbia 0"
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Contact: Josep
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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligomuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pWADA2 (gil 4/3/2114 [gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transfermed into chemically-competent B. coli XII.0-Gold (Stratagene) cells and selected for ampicillin resistance."
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/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
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/strain="Columbia On DNA"
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/strain="Columbia On DNA"
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/clone="Arabidopsis thaliana TDNA insertion lines"
/clone lib="Arabidopsis thaliana TDNA insertion lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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Spermatophyta, Magnollophyta, eudicotyledons; core eudicots; rosids
; eurosids II; Brassicales; Brassicaceae, Arabidopsis.

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A Sequence-Indexed Library of Insertion Mutations in the
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Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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(bases I to 25)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Josek, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P. A. Squence Indexed Library of Insertion Mutations in the
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/clone=lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
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Salk Institute Genomic Analysis Laboratory (SIGnAL)
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Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckerosalk.edu
This is single pass sequence recovered from the left border of
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0.005 inch orifice at constant velocity. The sheared DNA
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/strain="C57BL/6J"
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Insert Length: 10000 Std Erro
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Mus musculus
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Local 7; Conservative
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Fax: 801 585 7177
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Mesnen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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/clone_lib="Mouse lokb plasmid UdCcIM library"
/note="Vector: PWD42IV; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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84112, USA
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Insert Length: 10000 Std Error: 0.00
Plate: 0427 row: J column: 22
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/organism="Mus musculus"
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Class: plasmid ends
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University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0427J22"
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Fax: 801 585 7177
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was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWA2 (gil 4732114 |gb|AR129072.1), a copy.number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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University of Utah
University of Utah
University of Utah
Um. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mammoud, M., Meenen, B., Pedersen, T., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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2M0061122F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0061122 F, genomic survey sequence.
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/clone llb="Mouse lokb plasmid UGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Seq primer: CGTTGTAAAACGACGGCCAGT
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                                                                                           (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pware (pware) a copy-number inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli Xili0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 24)
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Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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100.0%; Pred. No. 2.3e+05;
tive 0; Mismatches 0;
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Insert Length: 10000 Std Error: 0
Plate: 0085 row: E column: 05
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC2M0085E05"
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Fax: 801 585 7177
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7; Conserv?
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwdy1472114[ph]AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xillo-Gold (stratagene) cells and selected for ampicillin resistance."
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yu01d01.rl Soares pineal gland N3HPG Homo sapiens cDNA clone IMAGE:232513 5' similar to SP:$36112 S36112 RETINOBLASTOMA-BINDING PROTEIN - ;, mRNA sequence.
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1 (bases 1 to 25)
1 Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,The WashU-Merck EST Project
                               /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
'clone lib="Mouse 10kb plasmid UUGC1M library"
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Possible reversed clone: similarity on wrong strand
Insert Length: 1325 Std Error: 0.00
Seq primer: M13RP1
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100.0%; Pred. No. 2.3e+05;
tive 0; Mismatches 0;
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/organism="Homo sapiens"
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/db_xref="GDB:3862504"
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Homo sapiens
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Best Local Similarity 100.09
Matches 7; Conservative
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Mus musculus (house mouse)
Mus musculus
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Matches 7; Conservative 0
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Fax: 801 585 7177
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,

Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.

1 (bases 1 to 24)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.

and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts
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Tel: 510 670 9338

Fax: 510 670 9302

Bmail: timbelynxgen.com
Sequence obtained from LYNX Therapeutics Megasort technology.

Collected from the down-regulated gate.

High quality sequence stop: 24.

Location/Qualifiers
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100.0%; Pred. No. 2.3e+05;
ative 0; Mismatches 0;
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0203 row: P column: 19
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/63"

    .24
    /organism="Homo sapiens"

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University of Utah Genome Center
University of Utah
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/clone="UUGC1M0203P19"
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Location/Qualifiers
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|q102114|gb|APL20072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Dunn,D., Aoyaj,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
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musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
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Insert Length: 10000 Std Error: (
Plate: 0298 row: J column: 20
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
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Location/Qualifiers
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Tel: 801 S85 5606
Fax: 801 S85 7177
Email: ddunmogenetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0462 row: J column: 10

Plate: 0462 row: J column: 10 Seg primer: CGTTGTAAAACGACGGCCAGT

Class: plasmid ends High quality sequence stop: 22.

Location/Qualifiers

source

FEATURES

/organism="Mus musculus"

us-09-540-843-7.szlm30.rst

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Contact: Burcham TS
LYNX Therapeutics, Inc.
25861 Industrial Blvd., Hayward, CA 94545, USA
                                                                                                                                                                                                   Laboratory Mouse DNA Resource
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                                                           /db_xref="taxon:10090"
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                                                                                                  /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.00
Thes 7; Conservative
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                                                                                                                                                                                      (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AR123072.1). a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli K110-Gold (Stratagene) cells
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC, UT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 22)
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1M0534H17R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC1M0534H17 R, genomic survey sequence.
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Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                   /clome_lib="Mouse 10kb plasmid UUGCIM library"
//note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/G7 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                              /lab_host="E. Coli strain_XL10-Gold, T1-resistant, F-"
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/mol_type="genomic DNA"
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Best Local Similarity 100.
Matches 7; Conservative
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11 AGTATGA 5
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwapto (giff) 4732114[p] AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xillo-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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                                                                                                    Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                 Plate: 0534 row: H column: 17
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                        organism="Mus musculus"
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Location/Qualifiers
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Plate: 0534 row: H c
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
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Length 22; 100.0%; Score 7; DB 28; 100.0%; Pred. No. 2.2e+05;

Gaps ö 0; Indels

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 24)
Evenner, S., Williams, S.R., Vermass, E.H., Storck, T., Moon, K., McCollum, C., Mao, J.I., Kirchner, J.J., Eletr, S., DuBridge, R.B., Burcham, T. and Albrecht, G.
In vitro cloning of complex mixtures of DNA on microbeads: Physical separation of differentially expressed cDNAs
Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000) AW059679 24 bp mRNA linear EST 23-AUG-2000 AHUTH.bsst.dnc15.aa.A050g08 DNC15 Homo sapiens cDNA, mRNA sequence. AW059679

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunch orifice at constant velocity. The sheared DNA was blunch end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMA2 (gql 4732114|gbl=A129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xillo-Gold (stratagene) cells and selected for ampicillin resistance."
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1M0462J10F Mouse 10kb plasmid UUGCIM library Mus musculus genomic . clone UUGCIM0462J10 F, genomic survey sequence.
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84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="Female"
/lab host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse lOkb plasmid UUGC2M library"
/note="Vebrary "PWD42vry PWD42vry"
musculus G57BL/6J (female) was obtained from the Jackson
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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                            Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0274 row: F column: 14
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
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University of Utah Genome Center
University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarese gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114 |gb|APL29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the innert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Malmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R.
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2M0274F14R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0274F14 R, genomic survey sequence.
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University of Utah Genome Center
University of Utah
Rm. 389, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
Tel: 801 585 5606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'lab_host="E: Coli strain XL10-Gold, T1-resistant, F-"
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/strain="C57BL/6J"
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/clone="UUGC2M0086E01"
                                                                                                                                                                    High quality sequence stop: 19.
Location/Qualifiers
   Email: ddunn@genetics.utah.edu
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
E 1 (bases 1 to 19)
S Dum, D. Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah
             AZ423817 1M0203919
AZ478673 1M0298720
AZ816652 2M0035505
H96935 Yu01d01.r1
AZ605844 1M0427J22
AZ802490 2M0061122
BH852866 SALK 0756
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BH856420 SALK 0797
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AL481025 T. Drucei
CZ1099 HUMGS000262
AL7698 ARABidops
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CZ1103 HUMGS000262
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AZ46698 ARABidops
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BG928185 HNC5-1-D
BG928195 HNC11-1-G
CZ1103 HUMGS000262
AI747751 u121h05.x
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AZ615402 1M044AL6
AZ656803 1M0966E09
AZ359199 1M0101M19
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AZ990856 2M0274F14
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AZ658158 1M0534H17
                                                                                               December 31, 2003, 13:58:09; Search time 804.291 Seconds (without alignments) 211.530 Million cell updates/sec
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            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                    nucleic search, using sw model
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Result Š.

polynucleotide, for therapeutic purposes, for studying expression and function of the polynucleotide and for expressing the phospholipase Novel isolated human Phospholipase A2, Group IB pancreas protein

Claim 19; Page 13; 51pp; English

The invention relates to an isolated human Phospholipase A2, Group IB (pancreas) (PLA2GIB) polymucleotide comprising a sequence which is a polymuchic variant for a reference sequence for the PLA2GIB gene or its fragment, or a polymuchic variant of a reference sequence for a the PLA2GIB gene of an individual, preddicting the haplotype pair for the PLA2GIB gene of an individual, preddicting the haplotype pair for the CLA2GIB cDNA or its fragment. Also included are haplotype pair for the PLA2GIB gene of an individual, identifying an association between a trait and at least one haplotype or haplotype pair of the PLA2GIB gene, an isolated genorching oligomoutlectide for detecting a polymorphism in the PLA2GIB gene, a recombinant non-human organism expresses a PLA2GIB gene, an isolated genome, where the organism expresses a PLA2GIB with the PLA2GIB sequence, where the organism expresses a PLA2GIB protein encoded by the first nucleotide sequence or by the polymorphic variant sequence, an isolated polypeptide comprising a sequence which is a polymorphic variant of a reference sequence for the PLA2GIB protein or transferted polymorphism data for the PLA2GIB monoclonal antibody, screening for drugs targeting PLA2GIB, a computer system for storing and analysing polymorphism data for the PLA2GIB gene and a genome anthology for PLA2GIB polymorphism data for the PLA2GIB gene and a genome anthology for PLA2GIB corputors of the PLA2GIB variant is useful in studying the efficiacy of therapeutic purposes. The transgenic crancer) and for testing the efficiacy of therapeutic agents and pancreatic cancer) and for therapeutic purposes. The transgenic organism is useful for studying expression of the PLA2GIB isogenes in vivo, for in vivo screening and testing of drugs targeted against PLA2GIB protein, and for testing the efficiacy of therapeutic agents and compounds in a biological several changing plA2GIB. The PLA2GIB sevel as on the binding all places of the pla2GIB section of the PLA2GIB sevel as well as on the binding of the plac polymorphisms in PLA2GIB. EEFFXEXERSCOSSSSSSSSSSSSSSSSSSSSSSSSSSSSS

Sequence 10 BP; 3 A; 3 C; 0 G; 4 T; 0 other;

Gaps ö 100.0%; Score 7; DB 24; Length 10; 100.0%; Pred. No. 5.7e+04; ive 0; Mismatches 0; Indels O Query Match 100.09

J. Best Local Similarity 100.09

Matches 7; Conservative 1 AGTATGA 7

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|||||||| AGTATGA 3

9 AGTATGA 3

Carrollered: December 31, 2003, 15:08:15

Mobilia : 202.291 secs

us-09-540-843-7.szlm30.rng

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The invention comprises peptide nucleic acid (PNA) oligomers, where the single units of the oligomers comprise different amino acid backbones selected from any amino acid, such as: including aminoethylglycine (aeg); aminoethylprolyl (aep); and aminoethylprolyl (aep); The PNA oligomers of the invention are useful for the downregulation of specific genes by targeting the genes at the mRNA or DNA level. The PNA oligomers are useful for treating bacterial and viral infections, cancer, metabolic diseases and immunological disorders. The PNA oligomers are also useful in PCR monitoring/modulation by PNA-clamping. The present DNA sequence represents a PNA oligomer of the invention.
                    /note= "This sequence is a peptide nucleic acid, (i.e. contains a polyamide backbone instead of a deoxyribose backbone"
                                                                                                                                                                                                                                                                                                                                                                    New peptide nucleic acid oligomer, useful as antisense molecules to treat bacterial and viral infections, has single units comprising different amino acid backbones such as aminoethylglycine -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10 BP; 2 A; 4 C; 0 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid microarray; probe; ss
                                                                                                                                                                                                                                                                                                                                                                                                                               Example 7; Page 34; 40pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid microarray probe #3
                                                                                 /*tag= b
/mod_base= OTHER
              mod_base= OTHER
                                                                                                                                                                                                                          24-NOV-2000; 2000DK-0001776.
06-MAR-2001; 2001DK-0000371.
16-JUL-2001; 2001DK-0001117.
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                                                                                                                                                                                                23-NOV-2001; 2001WO-DK00779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABK99556 standard; DNA; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
                                                                                                                                                                                                                                                                                                             Nielsen PE, Pueschl A;
                                                                                                                                                                                                                                                                                                                                        WPI; 2002-490198/52.
                                                                                                                                                                                                                                                                                    (PANT-) PANTHECO AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B AGTATGA 2
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                                                                                                                                          WO200242316-A2
                                                                      modified base
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Matches
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Gaps

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The invention relates to a nucleic acid array (I) comprising at least one hybridisation feature and at least one background feature. (I) is useful for detecting the presence of an analyte nucleic acid in a sample. The detection comprises contacting the nucleic acid array with the sample under stringent hybridisation conditions, subtracting the background corrected hybridisation signal to obtain a background corrected hybridisation signal and relating the background corrected hybridisation signal and relating the background corrected hybridisation signal and relating the background corrected hybridisation algoral to the presence of the analyte target nucleic acid in the sample analyte target nucleic acids present in the sample with a member of a signal producing system prior to contacting the array with the sample. ABK99529-ABK99544 and ABK99549-REF9578 represent nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; 88; primer; SNP; single nucleotide polymorphism; pancreatitis; pancreatic cancer; phospholipase A2 grouplB; PLAZG1B; gene therapy; haplotype; genotype; chromosome 12q23-q24.1; transgenic; drug screening; ASO; allele specific oligonucleotide; primer extension.
                                                                                                                                                                                  Nucleic acid arrays for qualitatively or quantitatively determining the presence of analyte target nucleic acid in a sample comprises both hybridisation features and background features -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 7; DB 24; Length 10; 100.0%; Pred. No. 5.7e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10 BP; 5 A; 1 C; 2 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                       Claim 8; Page 17; 38pp; English.
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ID ABK47394 standard; DNA; 10 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-AUG-2000; 2000US-223179P.
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              99US-0398399
                                                                                                                 Wolber PK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
1es 7; Conservative
                                            (DELE/) DELENSTARR G C. (WOLB/) WOLBER P K. (SANA/) SANA T R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kazemi A, Kliem SE,
                                                                                                                                                  WPI; 2002-582474/62.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the invention.
                                                                                                                 Delenstarr GC,
              17-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABK47394;
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Kinzler K;

us-09-540-843-7.szlm30.rng

WO200077214-A2.

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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previoually assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (3) a method (M2) for screening candidate attifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M2) for identifying human genes which are involved in cell cycle expression comprising contacting human DNA with a probe which comprises at least 10 contiguous nuclectides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell with a candidate drug and monitoring expression in the yeast cell with a candidate drug and monitoring expression in the yeast cell with call cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs.

The AFP135CB to AFF4064 the prepresent SAGE tags used in the exemplification of the cell cycle.
                                                                                                                                                                                                                                                                                                         Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    primers used in the SAGE method, in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the present invention. AAF33262 to AAF33267 represent linkers and PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 7; DB 22; Length 10; 100.0%; Pred. No. 5.7e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                           Example; Page 272; 419pp; English.
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                                                                                                                                                                                                                         Velculescu V, Vogelstein B,
                                                                                                 14-JUN-2000; 2000WO-US16223.
                                                                                                                                           99US-0335032
                                                                                                                                                                                 (UYJO ) UNIV JOHNS HOPKINS.
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                           16-JUN-1999;
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                                                           21-DEC-2000
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The invention relates to a method for detecting the presence and/or amount of a target nucleotide sequence in an analyte. The method comprising: contexting an aliquot of an analyte suspected of containing the target sequence with a set of features comprising oliophosphodiester probes; and subtracting a background signal from an observed signal to determine the presence and/or amount of the target sequence in the analyte. The method is used to detect the presence and/or amount of a target sequence in an analyte. The method is used for estimating background noise in a nucleic acid hybridisation assay and for validating a test-background feature. The method is useful in chemical, biological medical and diagnostic techniques, and for drug diacovery. The present sequence is a probe used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                             Detecting a target nucleotide sequence in an analyte, for use in e.g. drug discovery, comprises using a set of features having oligophosphodiester probes, and subtracting a background signal from an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PNA oligomer; PNA; peptide nucleic acid; polyamide backbone; ss; aminoethylglycine; aeg; aminoethylglycine; aeg; amorethylgrollidine; enterethylglycine; appectant infection; viral infection; cancer; metabolic disease; immunological disorder; PNA-clamping.
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                                                                                                                                                                                                                                                                         Sampras NM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 10;
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                                                                                                                                                                                                                                                                         Overman LB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 7; DB 24; I 100.0%; Pred. No. 5.7e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                       Lefkowitz SM, Luebke KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide nucleic acid (PNA) oligomer #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7; Page 19; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                      99US-0398399.
                                                                                                                    99US-0398399.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                      Delenstarr GC, Leinon-
-- IR, Wolber PK;
                                                                                                                                                 DELENSTARR G C.
                                                                                                                                                                  LEFKOWITZ S M.
                                                                                                                                                                                             OVERMAN L B.
SAMPRAS N M.
SAMPSON J R.
                                                                                                                                                                                                                                                                                                                  WPI; 2002-443693/47.
                                                                                                                                                                               LUEBKE K J.
                                                                                                                                                                                                                                          WOLBER P K.
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                           US2002051973-A1.
                                                                                                                                                                                                                                                                                                                                                                                           observed signal
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modified base
Unidentified.
                                                                                      17-SEP-1999;
                                                                                                                    17-SEP-1999;
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                                                         32-MAY-2002
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                                                                                                                                                (DELE/)
                                                                                                                                                                                                           (SAMP/)
                                                                                                                                                                               LUEB/
                                                                                                                                                                                                OVER/)
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Gaps ö

0; Indels

0; Mismatches

Target nucleotide, analyte, signal; drug discovery; probe, ss.

Probe #3 used to illustrate the method of the invention.

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SNINGOH SUHOC VINU ( OCYU)
                                                                         WPI; 2001-061874/07
                                     Velculescu V,
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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previoually assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a vest cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene as in M1; and (4) a method (M4) for identifying a candidate drug as a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affect phases of the cell cycle, the differentially expressed genes may be used to study, monitor and affect phases of the cell cycle, the cell cycle. The methods may be used as markers of phases of the cell cycle, and the differentially expressed genes may be used of an arkers of phases of the cell cycle, and feet the cell cycle, the cell cycle, and continued and per identification of an interventional continued and per identification of an intervention of a continued of AAF33268 to AAF44064 represent SAGE tags used in the exemplification of the present invention. AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle Example; Page 202; 419pp; English. XX
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VALOUS WENT
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YASAS GENE
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REAMPLE; F
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CC COMPINISH
GC COMPINISH

Sequence 10 BP; 4 A; 1 C; 3 G; 2 T; 0 other;

Gaps ; Length 10; 100.0%; Score 7; DB 22; Length 10 ilarity 100.0%; Pred. No. 5.7e+04; Conservative 0; Mismatches 0; Indels Local Similarity nes 7; Conserv

AAF39793 standard; DNA; 10 BP. AAF39793; 

RESULT 10

Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6532.

(first entry)

23-MAR-2001

Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.

Saccharomyces cerevisiae.

WO200077214-A2

21-DEC-2000

14-JUN-2000; 2000WO-US16223.

99US-0335032. 16-JUN-1999;

Kinzler

SNINGO UNIV JOHNS HOPKINS

Kinzler K; Velculescu V, Vogelstein B,

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle -

Example; Page 233; 419pp; English.

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previoually assigned open reading frame; or nonanocated ORF) genes comprising a SAGB (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, 5 phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast earl; and (b) monitoring expression of a noRF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M2) for identifying human genes which modifies the expression comprising contacting human DAM with a probe which comprises at least 10 contacting human plan are involved in cell cycle or identifying human genes which are involved in cell cycle or as in M1; and (4) a method (M4) for identifying a candidate drug as a candidate drug as a candidate drug and monitoring expression in the yeast cell of at least 10 contiguous nucleotides of a NORF gene whose expression waries or expression in a yeast cell comprising contacting a yeast cell of at least 10 condidate drug and monitoring expression in the yeast cell of at least 10 condidate expression in a yeast cell comprising contacting a yeast cell of at least 10 condidate in a yeast cell comprising contacting a yeast cell of at least 10 contacting expression in the yeast cell of the cell cycle. The methods may be used as markers of phases of the cell cycle. The differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs and provided the cell cycle identify candidate drugs and provided the cell cycle identify candidate drugs and provided the cell cycle identify candidate drugs and provided the cycle identify candidate of and suppose the cell cycle identify affect the cell cycle and for identification of antifungal drugs. AAF33268 to AAF44664 represent SAGE tags used in the exemplification of the present invention. AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present 

Sequence 10 BP; 4 A; 1 C; 2 G; 3 T; 0 other;

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Gaps ; 0 Length 10; 0; Indels 100.0%; Score 7; DB 22; L 100.0%; Pred. No. 5.7e+04; ive 0; Mismatches 0; Query Match Best Local Similarity 100...

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1 AGTATGA 7 ||||||| AGTATGA 7

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AAF40876 standard; DNA; 10 BP. RESULT 11 **AAF40876** 

23-MAR-2001 (first entry) AAF40876;

Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7615.

Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds. 

Saccharomyces cerevisiae

Human; metastatic breast tumour tissue; breast cancer; tag; primer; non-metastatic breast tumour tissue; gene therapy; anticancer; antimetastatic; vaccine; diagnosis; ss.

Homo sapiens WO9965928-A2

23-DEC-1999

us-09-540-843-7.szlm30.rng

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transcripts that are preferentially transcribed in the metastatic breast transcripts that are preferentially transcribed in the metastatic breast transcripts transcribts that are upregulated in metastatic breast transcripts.

AA2883942 to AA288677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic colls). AA2883942 to AA288677 represent tags corresponding to distinct transcripts that metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic blagnosis is by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected promoters from the transcripts are used to direct expression, in selected sequences), particularly an antigenenceded by the transcripts are also call-based vaccines. Polypeptides encoded by the transcripts are also useful in vaccines; (bot diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides can be used the expension of solate populations of educated, antigen encoding is or as therapeutic agents. Host cells that produce the polypeptides can be used of the expension of the expension of the educated, antigen encoding and controlled to the controlled of the encoded of the polypeptides can be used to expense.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to expand and isolate populations of educated, antigen-specific effecter cells, e.g. cytotoxic T lymphocytes, and these used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 7; DB 21; Length 10; 100.0%; Pred. No. 5.7e+04;
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Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prevention and treatment of cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 208; 219pp; English.
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98US-0090039.
98US-0090040.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Roberts BL, Shankara S;
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                                                                                                                                                                                                                                                                                                                                                                                                              (GENZ ) GENZYME CORP.
(ROBE/) ROBERTS B L.
(SHAN/) SHANKARA S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-106079/09.
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4 AGTATGA 10
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19-JUN-1998;
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AAH32760
ID AAH3
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The present invention describes an lipopolysaccharide (LPS) activated human monocyte expression gene group consisting of the highest expression among the genes expressed by human monocyte stimulated by LPS in which the CDNA of each gene has the base sequence of (AAH32628 to AAH32673) continuous to the base sequence 5'-CATG-3' nearest to the polyA region. The gene group is useful for the development of new means for the diagnosis and the treatment of various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human disease in which human monocyte plays an important role.

AAH35628 to AAH32943 represent specifically claimed LPS activated human monocyte expression gene cDNA tags from the present invention. AAH3294 represents an LPS activated human monocyte expression gene cDNA tags from the present invention. AAH3294 encoding AAB98009, which are given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                              Human, LPS, lipopolysaccharide; monocyte expression gene; tag; EST; expressed sequence tag; diagnosis; human disease; treatment; ss.
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                 LPS activated human monocyte expression gene cDNA tag SEQ:133.
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                                                                                                                                                                                                                                                                                                                                      LPS activated human monocyte expression gene group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10 BP; 4 A; 0 C; 4 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                      (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
                                                                                                                                                                                                                                                                                                                                                                         Claim 10; Page 28; 52pp; Japanese.
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                                                                                                    Homo sapiens.
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16-JUN-1999; 99US-0335032

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Gaps

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for DNA repair to occur before cell division takes place. The method is especially used to treat carcinoma but may also be used to: treat other hyperproliferative states (e.g. psoriasis or precancerous conditions); reduce photoaging, oxidative stress or damage; prevent skin cancer; treat allergically mediated inflammation (atopic or contact dermatitis, allergically mediated inflammation (atopic or reduce DNA damage in cells caused by radiation or chemicals; increase melanin production promote apoptosis in epithelial cells (e.g. for treating vitiligo), and to promote apoptosis in epithelial cells that contain damaged DNA. Also oligonucleotides that contain non-hydrolyzable backbones are used to inhibit apoptosis, in response to DNA damage, in epithelial cell in the sequence is melanogenesis associated oligonucleotides are used to oligonucleotides used to inhibit mammalian epithelial cell the proliferation, described in the method of the invention.
  resulting in transient arrest of cell growth, allowing more time
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAGE tag, serial analysis of gene expression; antigen-presenting cell; APC; monocyte-derived dendritic cell; differential gene expression; immunostimulatory cofactor; costimulatory factor; CTL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
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                                                                                                                                                                                                                              Sequence 9 BP; 3 A; 0 C; 4 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                     AAZ78995 standard; DNA; 10 BP
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98US-0089853.
98US-0089878.
98US-0089991.
98US-0089992.
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98US-00900000.
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98US-0090036.
98US-0090039.
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98US-0090042.
98US-0090043.
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Matches 7; Conservative
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complexion tages used to ladentity mived transcripts encoding cimumostimulatory cofactor proteins which are preferentially or differentially expressed in monocyte-derived dendritic cells compared with monocytes. Some of the transcripts correspond to known genes or stressed expense that services a variety or differentially expressed in dendritic cells, while preferentially or differentially expressed in dendritic cells, while cother transcripts correspond to novel genes. Antisque-presenting cell derivation of the cytotoxic immune response, particularly against tumour cells. Tumour antisque presentation via the MHC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone and subsequent recognition by T-cell receptors is alone insufficient to activate a robust cytotoxic immune response that can lyse the tumour cells, immunostimulatory coffactors also being required for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid sequences identified using the SAGE tags have several potential uses. They may be used in vaccines to induce an immune response, particularly expressed genes in a APC; and as hybridisation probes/amplification primers for the against a tumour antigen; to modulate the genotype of an APC; to an as hybridisation of the dendritic cell captoris and monitoring of diseases related to abnormal expression of these genes. Detection of their dendritic cell captoris and monitoring of diseases related to abnormal capteratially expressed genes, or of their encoded proteins, can be used in active immunotherapy (or to stimulate the genes can be used in active immunotherapy (or to stimulate the genes can be used in active immunotherapy (or to stimulate the presentation of co-stimulatory signals, migration to T cell-rich sites, co-captor cells or the presentation of co-stimulatory signals, migration to T cell-rich sites.
                                                                                                                                                                                                                                                                                                  Isolated polynucleotides differentially expressed in antigen-presenting cells, useful in gene vaccines against cancer -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Metastatic breast tumour cell downregulated transcript tag #5659.
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100.0%; Pred. No. 5.7e+04;
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                98US-0090077.
98US-0090078.
98US-0090079.
98US-0090080.
98US-0090076
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Best Local Similarity 10v...
7; Conservative
                                                                                                                                                                                                                    Roberts BL, Shankara S;
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ROBERTS B L.
SHANKARA S.
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19-JUN-1998;
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(ROBE/) F
(SHAN/) S
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23-NOV-1999 AAZ10692; Cobied to the control of the control

The invention describes inhibition of mammalian epithelial cell
proliferation by treating cells with at least one oligonucleotide, or
its fragment. The compounds, which have cytostatic, anti-allergic,
anti-inflammatcry, dermatclogical, ophthalmological, anti-psoriatic and
immunosuppressive activities, function as 'ultra-violet mimics' to induce
the property processes (or a protective response to later exposure to
radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
or a tumour necrosis factor inhibitor. Probably they mimic products of
the processed DNA-damage intermediates, by inducing the p53
pathway, resulting in transient arrest of cell growth, allowing more time
for DNA repair to occur before cell division takes place. The method is
for DNA repair to occur before cell division takes place. The method is
comparable to treat carcinoma but may also be used to: treat other
hyperproliferative states (e.g. psoriasis or precancerous conditions);
reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
allergically mediated inflammation (atopic or contact dermatitis,
allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in
cells caused by radiation or chemicals; increase melanin production
(pigmentation) in epithelial cells that contain damaged DNA, also
promote apoptosis in aptihelial cells that contain damaged DNA, also oligonuclectides that contain non-hydrolyzable backbones are used to inhibit apoptosis, in response to DNA damage, in epithelial cell. This sequence is melanogenesis associated oligonuclectide #7, one of the oligonuclectides used to inhibit mammalian epithelial cell proliferation, described in the method of the invention.

Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 other;

. 0 Length 7; 0; Indels 100.0%; Score 7; DB 23; I 100.0%; Pred. No. 3.7e+08; 0; Mismatches Query Match Best Local Similarity 100. Matches 7; Conservative

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Gaps

||||||| AGTATGA 7 AGTATGA 7

AAZ10692 standard; DNA; 9 BP.

(first entry)

Oligonucleotide sequence that increases p53 activity in a cell.

UV-induced hyperproliferative disease; psoriasis; vitiligo; atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging; skin cancer; ss. p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;

Synthetic

GB2336157-A

13-0CT-1999

99GB-0006758 24-MAR-1999; 98US-0048927 26-MAR-1998;

(UYBO-) UNIV BOSTON,

Gilchrest BA, Yaar M,

WPI; 1999-543520/46

DNA fragments useful for increasing p53 activity in a cell and reducing susceptibility to UV-induced hyperproliferative diseases -

Claim 11; Page 29; 44pp; English

AAZ10692-97 represent DNA fragments that are used for increasing p53

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention describes inhibition of mammalian epithelial cell proliferation by treating cells with at least one oligonucleotide, or its fragment. The compounds, which have cytostatic, anti-allergic, anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and immunosuppressive activities, function as 'ultra-violet mimics' to induce DNA repair processes (or a protective response to later exposure to radiation or chemicals), as a prollferation inhibitor, apoptosis inducer or a tumour necrosis factor inhibitor. Probably they mimic products of DNA damage, or processed DNA-damage intermediates, by inducing the p53
activity in a cell. The oligonucleotides are are UV mimetics and protect cells against subsequent exposure to UV irradiation or chemicals. The oligonucleotides are useful for increasing p53 activity in a cell, reducing the susceptibility to UV-induced hyperproliferative diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inhibiting proliferation of epithelial cells, useful e.g. for treating carcinoma, using specific oligonucleotides that mimic the effects of ultra-violet light
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                                                                                                                                                                                      Length 9;
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/note= "Optionally phosphorylated"
                                                                                                                                                                                  100.0%; Score 7; DB 20; I
100.0%; Pred. No. 2.9e+08;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Melanogenesis associated oligonucleotide #1.
                                                                                                            and reducing susceptibility to skin cancer.
                                                                                                                                                Sequence 9 BP; 3 A; 0 C; 4 G; 2 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                      AAS14905 standard; DNA; 9 BP.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                            2 AGTATGA
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The invention describes inhibition of mammalian epithelial cell proliferation by treating cells with at least one oligonucleotide, or lite fragment. The compounds, which have cytostatic, anti-allergic, anti-inflammatory, dermatological, obthalmological, anti-psoriatic and immunosuppressive activities, function as 'ultra-violet mimics' to induce DNA repair processes (or a protective response to later exposure to radiation or chemicals), as a proliferation inhibitor, apoptosis inducer or a tumour necrosis factor inhibitor. Probably they mimic products of DNA damage, or processed DNA-damage intermediates, by inducing the p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Melanin, melanogenic; oligomer; cytostatic; anti-allergic; p53; anti-inflammatory; dermatological; ophthalmological; anti-psoriatic; anti-inflammatory; dermatological; ophthalmological; anti-psoriatic; tumunosuppressive; DNA repair; proliferation inhibitor; apoptosis; tumour necrosis factor inhibitor; photoaging; hyperproliferative disease; carcinoma; oxidative stress; skin cancer; allergy mediated inflammation; conjunctivitis; allergic rhinitis; vitiligo; ss.
                                                                                                                                                                       AAZ10692-97 represent DNA fragments that are used for increasing p53 activity in a cell. The oligonucleotides are are UV minetics and protect cells against subsequent exposure to UV-irradiation or chemicals. The oligonucleotides are useful for increasing p53 activity in a cell, reducing the susceptibility to UV-induced hyperproliferative diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging and reducing susceptibility to skin cancer.
DNA fragments useful for increasing p53 activity in a cell and reducing susceptibility to UV-induced hyperproliferative diseases -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 7; DB 20; I 100.0%; Pred. No. 3.7e+08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 other;
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                                                                                                             Claim 11; Page 30; 44pp; English
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Matches 7;

Matches 7;

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Melanin; manunosup

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pathway, resulting in transient arrest of cell growth, allowing more time for DNA repair to occur before cell division takes place. The method is especially used to treat carcinoma but may also be used to: treat other the carcinoma but may also be used to: treat other carcinoma but may also be used to: treat other the precauce of the cancer of the cancer; treat allergically mediated inflammation (atopic or contact dermatitis, allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in calls caused by radiation or chemicals; increase melanin production (pigmentation) in epithelial cells that contain damaged DNA. Also oligonucleotides that contain non-hydrolyzable backbones are used to inhibit apoptosis, in response to DNA damage, in epithelial cell. This sequence is melanogenesis associated oligonucleotide #3, a truncated version of the oligonucleotide shown in AAS14906, one of the oligonucleotide shown in AAS14906, one of the oligonucleotide in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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/note= "Phosphorylated"
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Gaps ;

Length 7; 0; Indels Probe #3 used to i Peptide nucleic ac Nucleic acid micro Human PLA2G1B ASO Human GCNT1 allele

Human IL-8 gene po Human IL-8 gene po

gene SA gene SA gene SA

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ALIGNMENTS
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ABV6389
ABV6389
ABV6482
ABV66035
ABV66035
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ABV71010
ABV86037
ABV80877
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ABV80877
ABV80877
ABV80877
ABV80874
ABV71786
ABH731785
                              AAF40876
AAD44180
AAL44343
ABK49555
ABK47394
AAL41859
AAL67680
AAI67681
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                                                                                                                                                December 31, 2003, 11:36:21; Search time 202.291 Seconds (without alignments) 93.410 Million cell updates/sec
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| SIDSI/gcddata/geneseq/geneseqn-embl/NN1986.DAT:
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| SIDSI/gcddata/geneseq/geneseqn-embl/NN1989.DAT:
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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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Gapop 10.0 , Gapext 1.0
Gearched: 2552756 seqs, 1349719017 residues
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Raximum DB seq length: 30

Post-processing: Minimum Match 0*

Maximum Match 100*

Listing first 45 summaries
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Human maturation/a
Antisense oligonuc
Antisense oligonuc
Antisense oligonuc
Human skin EST 137
Human skin EST 322
Human skin EST 322
Human skin EST 362
Human skin EST 862
Human skin EST 137
Human skin ES

p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis; UV-induced hyperproliferative disease; psoriasis; vitiligo; atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging; skin cancer; ss. Oligonucleotide sequence that increases p53 activity in a cell Eller M; 99GB-0006758 98US-0048927 Gilchrest BA, Yaar M, (UYBO-) UNIV BOSTON 24-MAR-1999; 26-MAR-1998; GB2336157-A. 13-0CT-1999 Synthetic. 

WPI; 1999-543520/46

Melanogenesis asso Melanogenesis asso Oligonuclectide se Melanogenesis asso Human dendritic ce Metastatic breast LPS activated huma

AAS14911 AAS14905 AAS14905 AAZ78995 AAZ86425 AAH32760

100.0 100.0 100.0

AAZ10694 AAS14907

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Query Match Length

Score

Result ģ Oligonucleotide se

**Description** 

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BD085298 8 bp DNA linear PAT 27-AUG-2002 DNA-based transposon system for the introduction of nucleic acid
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NAL PREENT: JP 2001523450-A 10 27-NOV-2001;

REGENTS OF THE UNIVERSITY OF MINNESOTA
OS Artificial Sequence
ND 2001523450-A/10
PD 27-NOV-2001
PF 13-NOV-1999 US 60/065303
PI PERRY B HACKETT, KARL J CLARK, ADAM J DAPIE, STEVEN C EKAR, PI DAVID A LARJESPAYDA, ZOLTAN IBYCUS, TSSUSANNA ISSUFARK PC C12N15/09, A01K67/027, CO7K16/18, C12N5/10, C12Q1/68, C12N15/00, PC C DESCRIPTION OF Arrifinal COLOR DAVIDSON CC DESCRIPTION OF Arrifinal CC DESCRIPTION OF Arrifinal CC
                                                                                                                                                                                                                                                                                artificial sequences.

1 (bases 1 to 8)
Hackett, P.B., Clark, K.J., Dapie, A.J., Ekar, S.C., Larjespayda, D.A., Ibycus, Z. and Issufark, T.
DNA-based transposon system for the introduction of nucleic acid
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/organism='Artificial Sequence'
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="teaxon:32630"
/noTe="Synthetic DNA Fragment"
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    /db_xref="taxon:32630"

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1 (bases 1 to 8)
Messiaen, L. and Callens, T.
Improved mutation analysis of the nfl gene
Patent: Wo 0129251-A 224 26-APR-2001;
Location/Qualifiers
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/mol_type="genomic DNA"
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Tsuneyoshi,T., Westerhausen,A., Constantinou,C.D. and Prockop,D.J. Substitutions for glycine alpha 1-637 and glycine alpha 2-694 of type I procollagen in lethal osteogenesis imperfecta. The conformational strain on the triple helix introduced by a glycine substitution can be transmitted along the helix J. Biol. Chem. 266 (24), 15608-15613 (1991).
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Position dependent recognition of gnn nucleotide triplets by zinc
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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type I procollagen [human, mRNA Mutant, 9 nt]
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Patent: WO 0242459-A 2256 30-MAY-2002;
Sangamo Biosciences Inc. (US)
Location/Qualifiers
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Sequence 2256 from Patent WO0242459.
AX668807
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Position dependent recognition of gnn nucleotide triplets by zinc
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Position dependent recognition of gnn nucleotide triplets by zinc
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/mol_type="genomic DNA"
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Patent: WO 0242459-A 2220 30-MAY-2002;
Sangamo Biosciences Inc. (US)
Location/Qualifiers
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Patent: WO 0242459-A 623 30-MAY-2002;
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synthetic construct
artificial sequences.

1 (bases 1 to 10)
Della Valle, F., Callegaro, L. and Negro, A.
Process for the preparation of genetic vectors for the nerve growth factor expression in eukaryotic cells
Patent: EP 0432510-A 12 19-UUN-1991;
FIDIA S.P.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 9)

Tsuneyoshi,T., Westerhausen,A., Constantinou,C.D. and Prockop,D.J. Substitutions for glycine alpha 1-637 and glycine alpha 2-694 of type I procollagen in lethal osteogenesis imperfecta. The conformational strain on the triple helix introduced by a glycine substitution can be transmitted along the helix
J. Biol. Chem. 266 (24), 15608-15613 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 50585] from the original journal article. This sequence comes from Fig 5B.

Location/Qualifiers
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/organism="synthetic construct"
/mol type="genomic DNA"
/db_xref="taxon:32630"
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/gene="type I procollagen"
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/mol_type="genomic DNA"
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| SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
| SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
| SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
| SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
| SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
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                        GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Gapop 10.0, oagen. ...

Gapop 10.0, oagen. ...

Searched: 2552756 seqs, 1349719017 residues

Grotal number of hits satisfying chosen parameters:

Rinimum DB seq length: 0

Aximum DB seq length: 30

Gost-processing: Minimum Match 0*

Maximum Match 100*

Listing first 45 summaries
                                                                                                                            OM nucleic - nucleic search, using sw model
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UV-induced hyperproliferative disease; psoriasis; vitiligo; atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging; skin cancer; ss. p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis; Oligonucleotide sequence that increases p53 activity in a cell. Eller M; 99GB-0006758 98US-0048927 Gilchrest BA, Yaar M, (UYBO-) UNIV BOSTON 26-MAR-1998; 24-MAR-1999; GB2336157-A. 13-OCT-1999. Synthetic. 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

WPI; 1999-543520/46

Oligonuclectide se Oligonuclectide se Melanogenesis asso Melanogenesis asso Oligonuclectide se Melanogenesis asso Melanogenesis asso Direct repeat sequ

AAS14908 AAS14910 AAZ10694 AAS14907 AAS14911

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AAZ10695 AAZ10696

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Query Match Length

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Description

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0; Mismatches

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AAZ10692-97 represent DNA fragments that are used for increasing p53 activity in a cell. The oligonucleotides are are UV mimetics and protect cells against subsequent exposure to UV-irradiation or chemicals. The oligonucleotides are useful for increasing p53 activity in a cell, reducing the susceptibility to UV-induced hyperproliferative diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging and reducing susceptibility to skin cancer.
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Melanin, melanogenic; oligomer; cytostatic; anti-allergic; p53; anti-inflammatory; dermatological; ophthalmological; anti-psoriatic; immunosuppressive; DNA repair; proliferation inhibitor; apoptosis; tumour necrosis factor inhibitor; photoaging; hyperproliferative disease; carcinoma; oxidative stress; skin cancer; allergy mediated inflammation; conjunctivitis; allergic rhinitis; vitiligo; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inhibiting proliferation of epithelial cells, useful e.g. for treating carcinoma, using specific oligonucleotides that mimic the effects of ultra-violet light
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                                                                                                                                                                                                                                  AAS14908 standard; DNA; 5 BP.
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                                                                                                                                                                                                                              diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging
                                                                                                                                            activity in a cell. The oligonucleotides are are UV mimetics and protect cells against subsequent exposure to UV-irradiation or chemicals. The oligonucleotides are useful for increasing p53 activity in a cell, reducing the susceptibility to UV-induced hyperproliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA fragments useful for increasing p53 activity in a cell and reducing susceptibility to UV-induced hyperproliferative diseases -
         DNA fragments useful for increasing p53 activity in a cell and reducing susceptibility to UV-induced hyperproliferative diseases -
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                                                                                                                        AAZ10692-97 represent DNA fragments that are used for increasing p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis; UV-induced hyperproliferative disease; psoriasis; vitiligo; atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;
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                                                                                                                                                                                                                                                                         and reducing susceptibility to skin cancer.
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                                                                             Claim 11; Page 30; 44pp; English
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PT DNA fragments useful for increa susceptibility to UV-induced hy. XX
Claim 11; Page 30; 44pp; Englis XX
AA10692-97 represent DNA fragment cc cerivity in a cell. The oligomucic or cemicals. The oligomucicides in a cell, reducing the susception of the condition of the condition
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Eller M;

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The invention describes inhibition of mammalian epithelial cell

proliferation by treating cells with at least one oligonucleotide, or

the fragament. The compounds, which have exposetatic, anti-allergic,

anti-inflammatory, dermatological, ophthalmological, anti-allergic

anti-inflammatory, dermatological, ophthalmological, anti-allergic and

immunosuppressive activities, function as 'ultra-violet mimics' to induce

to an tumour necrosis factor inhibitor. Probably they mimic products of

DNA damage, or processed DNA-damage intermediates, by inducing the p53

cor a tumour necrosis factor inhibitor. Probably they mimic products of

DNA damage, or processed DNA-damage intermediates, by inducing the p53

pathway, resulting in transient arrest of cell growth, allowing more time

for DNA repair to occur before cell division takes place. The method is

cor byperproliferative states (e.g. psoriasis or precancerous conditions);

reduce photoaging, oxidative stress or damage; prevent skin cancer; treat

allergically mediated inflammation (atopic or contact dermatitis,

allergically mediated inflammation (atopic or contact dermatitis,

allergically mediated inflammation (atopic or contact dermatitis,

cells caused by radiation or chemicals; increase melanin production

(pigmentation) in epithelial cells (e.g. for treating vitiligo), and to

colls acused by radiation or chemicals; increase melanin production

(pigmentation) in epithelial cells (e.g. for treating vitiligo), and to

colls equence is melanogenesis associated oligonucleotide #4, a truncated

version of the oligonucleotide shown in manalian epithelial cell

colligration, described in the method of the invention.
Claim 1; Page 36; 74pp; English.
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100.0%; Score 5; DB 20; Length 5;

Query Match

Gaps

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Length 5; Indels

Score 5; DB 23; I Pred. No. 5.2e+08;

0; Mismatches

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Sequence 5 BP; 2 A; 2 C; 0 G; 1 T; 0 other;
    described in the method of the invention.
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Matches
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ID AAS1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention describes inhibition of mammalian epithelial cell proliferation by treating cells with at least one oligonucleotide, or its fragment. The compounds, which have cytostatic, anti-allergic, anti-inflammatory, dermatological, onthalmological, anti-psoriatic and immunosuppressive activities, function as 'ultra-violet minics' to induce DNA repair processes (or a protective response to later exposure to radiation or chemicals), as a proliferation inhibitor, apoptosis induce or a tumour necrosis factor inhibitor. Probably they mimic products of DNA damage, or processed DNA-damage intermediates, by inducing the p53 pathway, resulting in transient arrest of cell growth, allowing more time for DNA repair to occur before cell division takes place. The method is especially used to treat carcinoma but may also be used to: treat other
                                                                                                                                                                                                                                                                                                                                                   anti-inflammatory; dermatological; ophthalmological; anti-psoriatic; immunosuppressive; DNA repair; proliferation inhibitor; apoptosis; tumour necrosis factor inhibitor; photoaging; hyperproliferative disease; carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hyperproliferative states (e.g. psoriasis or precancerous conditions); reduce photoaging, oxidative stress or damage; prevent skin cancer; treat allergically mediated inflammation (atopic or contact dermatitis, allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in cells caused by radiation or chemicals; increase melanin production (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to promote apoptosis in epithelial cells that contain damaged DNA. Also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oligonucleotides that contain non-hydrolyzable backbones are used to inhibit apptosia, in response to DNA damage, in repithelial cell. This sequence is melanogenesis associated oligonucleotide #6, one of the oligonucleotides used to inhibit mammalian epithelial cell proliferation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inhibiting proliferation of epithelial cells, useful e.g. for treating carcinoma, using specific oligonucleotides that mimic the effects of ultra-violet light \, -
                                                                    Gaps
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                                 100.0%; Score 5; DB 23; Length 5; 100.0%; Pred. No. 5.2e+08; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        conjunctivitis; allergic rhinitis; vitiligo; ss.
                                                                                                                                                                                                                                                                                                      Melanogenesis associated oligonucleotide #6.
Sequence 5 BP; 1 A; 0 C; 2 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 36; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eller M;
                                                                                                                                                                                                            AAS14910 standard; DNA; 5 BP.
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                                                                                                                                                                                                                                                                          (first entry)
                                                 Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
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                                 Query Match
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AAS14910/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA fragments useful for increasing p53 activity in a cell and reducing susceptibility to UV-induced hyperproliferative diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                          p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis; UV-induced hyperproliferative disease; psoriasis; vitiligo; atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;
                                                                                                                                                                                                                     Oligonucleotide sequence that increases p53 activity in a cell.
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AAZ10694 standard; DNA; 7 BP
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                                                                                                                                           23-NOV-1999 (first entry)
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Query Match
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Melanin, melanogenic; oligomer; cytostatic; anti-allergic; p53; anti-inflammatory; dermatological; ophthalmological; anti-psoriatic; anti-inflammatory; dermatological; ophthalmological; anti-psoriatic; tumunosuppressive; DNA repair; proliferation inhibitor; apoptosis; tumour necrosis factor inhibitor; photoaging; hyperproliferative disease; carcinoma; oxidative stress; akin cancer; allergy mediated inflammation; conjunctivitis; allergic rhinitis; vitiligo; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inhibiting proliferation of epithelial cells, useful e.g. for treating carcinoma, using specific oligonucleotides that mimic the effects of ultra-violet light -
                                                                                                                                                                       Melanogenesis associated oligonucleotide #7.
                         AAS14911 standard; DNA; 7 BP
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modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                        AAS14911;
AAS14911
                         The invention describes inhibition of mammalian epithelial cell proliferation by treating cells with at least one oligonucleotide, or lits fragment. The compounds, which have cytostatic, anti-albragic, anti-inflammatory, dermatological, ophthalmological, anti-albragic, anti-inflammatory, dermatological, ophthalmological, anti-inflammatory dermatological, ophthalmological, anti-albragic and immunosuppressive activities, function as 'ultra-violet mimics' to induce DNA repair processes (or a protective response to later exposure to radiation or chemicals), as a proliferation inhibitor, apoptosis inducer or a tumour necrosis factor inhibitor. Probably they mimic products of DNA damage, or processed DNA-damage intermediates, by inducing the p53 pathway, resulting in transient arrest of cell growth, allowing more time for DNA repair to occur before cell division takes place. The method is especially used to treat carcinoma but may also be used to: treat other hyperproliferative streats (e.g. psoriasis or precancerous conditions); reduce photoaging, oxidative stress or damage; prevent skin cancer; treat allergically mediated inflammation (atopic or contact dermatitis, allergically mediated inflammation (atopic or contact dermatitis, allergic rhinitis and conjunctivitis); prevent or reduce DNA, and to colligonucleotides that contain non-hydrolyzable backbones are used to inhibit apoptosis, in response to DNA damage, in epithelial cells that contain damaged by the contain non-hydrolyzable backbones are used to inhibit apoptosis, in response to DNA damage, in epithelial cells every of the oligonucleotide shown in AASI4906, one of the oligonucleotide shown in AASI4906, one of the oligonucleotide so the inhibit mammalian epithelial cell
                                                                                                                                           Melanin, melanogenic; oligomer; cytostatic; anti-allergic; p53; anti-inflammatory; dermatological; ophthalmological; anti-psoriatic; ammunosuppressive; DNA repair; proliferation inhibitor; apoptosis; tumour necrosis factor inhibitor; photoaging; hyperproliferative disease; carcinoma; oxidative stress; skin cancer; allergy mediated inflammation; conjunctivitis; allergic rhinitis; vitiligo; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inhibiting proliferation of epithelial cells, useful e.g. for treating carcinoma, using specific oligonuclectides that mimic the effects of ultra-violet light
                                                                                               Melanogenesis associated oligonucleotide #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 36; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAR-2001; 2001WO-US10162
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                                              (first entry)
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                                                                                                                                                                                                                                                                                                                        Synthetic
AAS14907
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Eller M;

/note= "Phosphorylated"

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Location/Qualifiers

(first entry)

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proliferation by treating cells with at least one oligonucleotide, or its fragment. The compounds, which have cytostatic, anti-placegic, arti-inflammentory, dermatological, anti-psoriatic and immunosuppressive activities, function as 'ultra-violet mimics' to induce immunosuppressive activities, functions a' ultra-violet mimics' to induce cradiation or chemicals), as a proliferation inhibitor. Probably they mimic products of DNA damage, or processed DNA-damage intermediates, by inducing the p53 cor a tumour necrosis factor inhibitor. Probably they mimic products of DNA damage, or processed DNA-damage intermediates, by inducing the p53 cor processed DNA-damage intermediates, by inducing the p53 cor processed DNA-damage intermediates, by inducing the p53 cor processed DNA-damage in transient arrest of call growth, allowing more time for DNA repair to occur before call division takes place. The method is especially used to treat carcinoma but may also be used to: treat other corpustions or precancerous conditions); reduce photoaging, oxidative stress or damage; prevent skin cancer; treat allergically mediated inflammation (atopic or contact dermatitis, allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in calls caused by radiation or chemicals; increase melanin production corpus approach apoptocial calls calls that contain damaged DNA, also promote apoptocial calls calls calls contain damaged DNA, also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oligonuclectides that contain non-hydrolyzable backbones are used to inhibit apoptosis, in response to DNA damage, in epithelial cell. This sequence is melanogenesis associated oligonucleotide #7, one of the oligonucleotides used to inhibit mammalian epithelial cell proliferation, described in the method of the invention.
                                                                                                                           invention describes inhibition of mammalian epithelial cell
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Claim 1; Page 38; 74pp; English.
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Score 5; DB 23; Length 7; Pred. No. 3.7e+08;

100.0%;

Query Match Best Local Similarity

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Gaps ; 0

Length 7; 0; Indels

100.0%; Score 5; DB 23; I 100.0%; Pred. No. 3.7e+08; tive 0; Mismatches 0;

Best Local Similarity 100. Matches 5; Conservative

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GTATG

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RESULT 7

Gaps

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Length 8; Indels

Matches

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(MHC) class I and class II antigen expression and expression of other antigens, the gene promoters of which contain related sequence motifs that are stimulated by the same factors which stimulate MHC class I and class II antigen expression. Such utrons can be used to regulate gene expression in a subject, e.g. a human or a cell in vitro, specifically inhibiting MHC class I or II, ICAM-7, B7-1, B7-2, FC gamma R, IL-2 or HIV gene expression. They can be used to inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transplant rejection, or treat an autoimmune or inflammatory disease or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a promoter regulatory element, found in the utrons of the invention. Utrons are from, or are homologous to, the 3' untranslated region (UTR), of an mRNA that stimulates or inhibits a cellular response by sequence specific interactions. The utron is able to suppress constitutive and interferon-gamma (IFN-gamma) induced major histocompatibility complex
                                                                                                                                                                                                                                                                                                                                               3' untranslated region; UTR; inhibition; gene expression; ICAM-7; interferon-gamma; IFN-gamma; major histocompatibility complex; MHC; antigen expression; gene promoter; utron; B7-1; B7-2; Fc gamma R;
                                                                                                                                                                                                                                                                                                               A promoter regulatory motif found in the utrons of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Utrons, RNA molecules containing promoter regulatory motifs -useful to suppress express expression from promoter of interest, specifically TSU nucleic acid suppression of MHC Class I and II
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   DB 22; L
3.2e+08;
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60.0%; Pred. No. 2.9e+08;
ive 2; Mismatches 0;
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                                       0; Mismatches
   100.0%; Score 5; 100.0%; Pred. No.
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                                                                                                                                                                                                       AAV22350 standard; RNA; 9 BP
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Best Local Similarity 60.07
المالية 3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified.
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                                                                                                                                                                                                                                                                           29-JUN-1998
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                      Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The patent discloses non-integrating viral vectors comprising a polymucleotide flanked by inverted repeats that bind a transposase, a transposase-encoding polymucleotide operably linked to a regulatory sequence comprising an operator, that alters expression of the ransposase-encoding polymucleotide. Transposon sequences can integrate into genemic DNA whether or not the cell is dividing. AGSB10 is a SB (Sleeping Beauty) transposae-transducing adenoviral non-integrating vector. The non-integrating viral vectors are useful for treating vector. The non-integrating viral vectors are useful for treating vector. The non-integrating viral vectors are useful for treating vector. The non-integrating viral vectors are useful for treating control of supplementation of a metabolic activity. These genetic disease characterised by subnormal production of a polypeptide or brain malfunction. The non-integrating viral vectors are useful as nucleic acid delivery systems, e.g. for genome analysis or gene therapy and can also be used for applications that involve long-term production of a polypeptide. The non-integrating viral vectors are also useful for creating transgenic host cells that provide normal cells with protection against toxic side effects of chemotherapy.

The sequence of the present invention is a direct repeat sequence that
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Non-integrating (adenovirus-based) viral vectors useful in gene therapy, especially for treating patients suffering from a genetic disease, e.g. cystic fibrosis, diabetes, cardiovascular disease, cancer or brain malfunction -
                                                                                                                                                                                                                                                                                                                            non-integrating viral vector; cytostatic; anti-diabetic; cardiant; neuroprotective; genetic disease; gene therapy; therapy; cancer; cystic fibrosis; diabetes; cardiovascular disease; brain malfunction; genome analysis; chemotherapy; transgenic host cell; direct repeat; ds.
 Gaps
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 0; Indels
                                                                                                                                                                                                                                                                                                           Sleeping Beauty; SB; AdSB10; adenovirus; transposase;
                                                                                                                                                                                                                                                                         Direct repeat sequence that binds to SB protein.
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Mismatches
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                                                                                                                                                              AAD02250 standard; DNA; 8
5; Conservative
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                                                                                                                                                                                                                                     28-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified
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Length 9;

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Sequence 9 BP; 3 A; 0 C; 3 G; 3 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYYA ) UNIV YALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9744450-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-NOV-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peyman JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
RESULT 10
AAV22283
ID AAV22283
XX AAV22283
XX AAV22283
XX AAV22
XX AAV22
XX BASS
XX B
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This is a nonamer consensus sequence of a cyclin D transcription factor

DMP1. DMP1 is an amino acid polymer which has binding affinity for a
D-type cyclin, in vitro, and for a specific DNA mucleotide sequence and
is a transcription factor involved in the activation of genes that
prevent cell proliferation. The DMP1 nucleic acid is operatively linked
to an expression control sequence on an expression vector. The expression
vector has a transcription control sequence comprising this nonamer
sequence operably associated with a recombinant gene or a cassette
insertion site for a recombinant gene. The vector is homologoually
recombined in a chromosome of a transgenic animal. A probe or a
competitor in DMP1 transactivation assays is designed based on this
competitor in DMP1 transactivation assays is designed based on this
competitor in DMP1 transactivation assays is designed based on this
competitor in DMP1 the probe under conditions that allow binding of the
from a mammal with the probe contains the core sequence GTA, and where
the presence or activity of DMP1 is suspected in the sample. DMP1 can
function as a cell cycle inhibitor when expressed in a tumour cell.
Modulating the expression of DMP1 can be used to treat tumour cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancers. DMP1 can also be used for controlling expression of heterologous proteins. Antisense sequences and ribozymes can be used to inhibit expression of the transcription factor. Detecting the level and activity of DMP1 in cells is useful for detection of cancer cells or
                                                                                                                                                                                                                                                   cyclin D transcription factor; binding affinity; D-type cyclin; probe; cell cycle inhibitor; tumour; detection; cancer; DMP1; competitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cyclin D transcription factor and related DNA - can be used to develop products for treatment of, e.g. cancer
                                                                                                                                                                                                   Cyclin D transcription factor DMP1 nonamer consensus sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 99; 120pp; English.
                                                                                                                                                                                                                                                                                                                    nonamer consensus sequence; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hirai H, Inoue K, Sherr CJ;
                          AAV15899 standard; DNA; 9 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0017815.
96US-0017815.
96US-0648837.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97WO-US08480.
                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dysproliferative cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-008884/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09743415-A1
                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-MAY-1997;
                                                                                                                                           26-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L5-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-MAY-1996;
16-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-NOV-1997.
                                                                                   AAV15899;
AAV15899
                                                                                The present sequence represents a GAS complement gene promoter motificand in a trophoblast STAT utron (TSU). TSUS be isolated from a CDNA library prepared from mRNA isolated from trophoblast cells. Utrons are from, or are homologous to, the 3' untranslated region (UTR), of an mRNA that stimulates or inhibits a cellular response by sequence specific interfactions. The TSU is able to suppress constitutive and interfacton-gamma (IRN-gamma) induced major histocompatibility complex (MHC) class I and class II antigen expression and expression of other antigens, the gene promoters of which contain related sequence motifis that are stimulated by the same factors which stimulate MHC class I and class II antigen expression. The TSU sequence contains motifis related to IRN afgnalling (GAS, ISRE and interleukin-4 response elements). The nucleic acid can be used to regulate gene expression in a subject, e.g. a human or a cell in vitro, specifically inhibiting MHC Class I or II, can be used to inhibit transplant rejection, or treat an autoimmune or used to inhibit the
                                                                                                                                                                                                                                                                                                                                                                      interferon-gamma; IFN-gamma; major histocompatibility complex; MHC; antigen expression; gene promoter; class I; class II; IFN signalling; GAS; ISRB; interleukin-4 response element; gene expression; ICAM-7; B7-2; FC gamma R; HIV gene expression; transplant rejection; treatment; autoimmune disease; inflammatory disease; ss.
                                                                                                                                                                                                                                                                                                                                               Trophoblast STAT utron; TSU; 3' untranslated region; UTR; inhibition;
                                                                                                                                                                                                                                                                                   GAS complement gene promoter motif found in a trophoblast STAT utron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Utrons, RNA molecules containing promoter regulatory motifs -useful to suppress expression from promoter of interest, specifically TSU nucleic acid suppression of MHC Class I and II gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 22; Page 90; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     action of STAT1-6, or a cytokine.
                                                                                                                AAV22283 standard; DNA; 9 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97WO-US09459.
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                                                  Gaps
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                        100.0%; Score 5; DB 19; Length 9; 100.0%; Pred. No. 2.9e+08;
                                                0, Indels
Sequence 9 BP; 1 A; 3 C; 2 G; 3 T; 0 other;
                                                  0; Mismatches
                                    Local Similarity 100.
                                                                           1 GTATG 5
                         Query Match
                                     Best Loca
Matches
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Gaps

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100.0%; Score 5; DB 19; Length 9; 100.0%; Pred. No. 2.9e+08; ive 0; Mismatches 0; Indels

5; Conservative

Matches

1 GTATG 5 GTATG 5

RESULT 11

RESULT 12

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Location/Qualifiers
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                                                                                                                                                                           30-MAR-2001; 2001WO-US10162
                                                                                                                                                                                                          31-MAR-2000; 2000US-0540843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-JAN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human DNA PCR primer #15.
                                             '*tag=
                                                                                                                                                                                                                                                                          Yaar M,
                                                                                                                                                                                                                                                                                                        WPI; 2001-626338/72.
                                                                                                                                                                                                                                          (UYBO-) UNIV BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GTATG 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 GTATG 7
                                                                                                            WO200174342-A2
                Key
modified_base
                                                                                                                                                                                                                                                                          Gilchrest BA,
                                                                                                                                           11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Matches
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8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEXTXEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Melanin, melanogenic; oligomer; cytostatic; anti-allergic; p53; anti-inflammatory; dermatological; ophthalmological; anti-psoriatic; immunosuppressive; DNA repair; proliferation inhibitor; apoptosis; tumour necrosis factor inhibitor; photoaging; hyperproliferative disease; carcinoma; oxidative stress; skin cancer; allergy mediated inflammation; conjunctivitis; allergic rhinitis; vitiligo; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ10692-97 represent DNA fragments that are used for increasing p53 activity in a cell. The oligonucleotides are are UV minetics and protect cells against subsequent exposure to UV-irradiation or chemicals. The oligonucleotides are useful for increasing p53 activity in a cell, reducing the susceptibility to UV-induced hyperproliferative diseases, treating psoriasis, viciligo, atopic dermatitis, allergic rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging and reducing susceptibility to skin cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA fragments useful for increasing p53 activity in a cell and reducing susceptibility to UV-induced hyperproliferative diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                        UV-induced hyperproliferative disease, psoriasis, vitiligo, atopic dermatitis, allergic rhinitis, conjunctivitis, photoaging, skin cancer, ss.
                                                                                                                                         p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;
                                                                                                         Oligonucleotide sequence that increases p53 activity in a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 5; DB 20; Length 9; 100.0%; Pred. No. 2.9e+08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Melanogenesis associated oligonucleotide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9 BP; 3 A; 0 C; 4 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; Page 29; 44pp; English
           AAZ10692 standard; DNA; 9 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAS14905 standard; DNA; 9 BP
                                                                                                                                                                                                                                                                                                                      99GB-0006758.
                                                                                                                                                                                                                                                                                                                                                      98US-0048927
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                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    Gilchrest BA, Yaar M,
                                                                                                                                                                                                                                                                                                                                                                                    (UYBO-) UNIV BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-543520/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GTATG 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTATG 7
                                                                        23-NOV-1999
                                                                                                                                                                                                                                                                                                                      24-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                      26-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-FEB-2002
                                                                                                                                                                                                                                                      GB2336157-A
                                                                                                                                                                                                                                                                                      13-OCT-1999
                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                         AAZ10692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAS14905;
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The invention describes inhibition of mammalian epithelial cell

cris fragment. The compounds, which have cytostatic, anti-allergic,

anti-inflammatory, dermatological, ophthalmological, anti-allergic,

anti-inflammatory, dermatological, ophthalmological, anti-allergic,

anti-inflammatory, dermatological, ophthalmological, anti-allergic and

immunosuppressive activities, function as 'ultra-violet mimics' to induce

con a tumour necrosis factor inhibitor. Probably they mimic products of

con a tumour necrosis factor inhibitor. Probably they mimic products of

con a tumour necrosis factor inhibitor. Probably they mimic products of

con a tumour necrosis factor inhibitor. Probably they mimic products of

con a tumour necrosis factor inhibitor. Probably they mimic products of

con a tumour necrosis factor inhibitor. Probably they mimic products of

con a tumour necrosis factor inhibitor. Probably they mimic products of

con a tumour necrosis factor inhibitor. Probably they mimic products of

con a tumour necrosis factor inhibitor and may also be used to: treat carcinoma but may also be used to inhibit apoptosis in epithelial cells (e.g. for treating vitiligo), and to

contact callergic rhinitis and conjunctivitis); prevent or reduce DNA damage in

colls caused by radiation or chemicals; increase melanin production

copyromote apoptosis in epithelial cells (e.g. for treating vitiligo), and to

contact anone apoptosis in response to DNA damage, in epithelial cells (e.g. for treating vitiligo), and to

contact anone apoptosis in response to DNA damage, in epithelial cells (e.g. for contact contain damaged by

contact centact contain non-hydrolyzable backbones are used to

contact centact contain non-hydrolyzable backbones of the

colligonucleotides used to inhibit mammalian epithelial cell in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inhibiting proliferation of epithelial cells, useful e.g. for treating carcinoma, using specific oligonucleotides that mimic the effects of ultra-violet light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
/mod_base= g
/note= "Optionally phosphorylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9 BP; 3 A; 0 C; 4 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eller M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 36; 74pp, English.
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RESULT 13

9/20d4<sup>8</sup>

sapiens.

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The invention relates to a differential display comprising contacting cDNA with a first primer that hybridises to an oligonucleic sequence couling for a leucine-rich motif, and with a second oligonucleotide primer to form a cDNA-hybrid molecule. The method comprises obtaining mRNA from at least 2 samples, synthesising cDNA from the RNA of each sample, contacting the cDNA with a first primer that hybridises to an oligonucleotide primer to form a leucine-rich motif, and with a second oligonucleotide primer to form cDNA-hybrid molecules, detecting amplified products and comparing the amplified products from each sample to identify distinctive amplified products coding for at least one secreted or transmembrane protein. The method is useful for discovering novel secreted and/or transmembrane proteins which are important for cell processes and play an important role in determining its phenotype, and which act as mediators for the transfer of signals from expression. Sequences ABX03772-ABX03790 represent PCR primers used in the differential display method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                 Differential display method for identifying secreted or transmembrane protein, comprises contacting a DNA with a first primer that hybridizes to a sequence coding for a leucine-rich motif and with a second oligonucleotide primer -
Differential display method; leucine-rich motif; transmembrane protein;
secreted protein; primer; PCR; ss; human.
                                                                                                                                                                                                                                                                                   (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9 BP; 1 A; 0 C; 2 G; 2 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 52; Page 17; 37pp; English.
                                                                                                                                                                                                      23-JAN-2002; 2002WO-IL00071.
                                                                                                                                                                                                                                             23-JAN-2001; 2001US-263158P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-599769/64.
                                                                                                                        WO200259259-A2
                                                                                                                                                                                                                                                                                                                          Wreschner DH;
                                                                                                                                                              01-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Si
OMatches 5;
                                                                                   Synthetic
                                                                Homo
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that it binds to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target subsites having the nucleotide G in the 5'-most position of the subsite. (I) is useful in studying gene function, and for human therapeutic methods to modulate the expression of a target region within a subject, in diagnostic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determined the phenotype and function of gene expression. (I) has improved affinity and specificity for their target sequences, as well as enhanced biological activity. ABQ71211 to ABQ72214 and ABP48191 to ABSF1230 represent DNA target sequences and zinc finger peptides which are given
                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a zinc finger protein (1) that binds to a target site, comprising a first (F1), a second (F2), and a third (F3) zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the target site comprises, in 3-5-5 direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (1) a polypeptide (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and (S3) designing (M) (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, selecting the F2 zinc finger such
                                                                                                                                                                                                                                                               New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 5; DB 24; I 100.0%; Pred. No. 2.9e+08; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9 BP; 2 A; 2 C; 3 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: December 31, 2003, 15:08:14 Job time : 145.494 secs
                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 45; 81pp; English.
                                                                                                                                   (SANG-) SANGAMO BIOSCIENCES INC.
                                           20-NOV-2001; 2001WO-US43438
                                                                                     20-NOV-2000; 2000US-0716637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100...
5, Conservative
                                                                                                                                                                                                                      WPI; 2002-500284/53.
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30-MAY-2002
                                                                                                                                                                                                                                                                                                                                    C-terminus
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primer

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Gaps

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100.0%; Score 5; DB 24; Length 9; 100.0%; Pred. No. 2.9e+08; rive 0; Mismatches 0; Indels

1 GTATG 5 GTATG 9 Zinc finger protein related oligonucleotide target SEQ ID NO:623 Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.

us-09-540-843-4.szlm30.rst

OM nucleic

Run on:

Sequence:

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BG928185 HNC65-1-D
BG929060 HNC11-1-G
BG55681 E012692-0
C21103 HUMGS000262
BM397954 5009-0-39
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A1120725 ub72711.r
A17751 u121h05.x
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AZ345849 IM0080D16
AZ452163 IM0206B22
AZ46513 IM0276G12
AZ44551 IM0274G11
AZ44851 IM0274G11
AZ486152 IM0314A04
AZ65685 IM0314A04
AZ65685 IM0467M01
AZ656685 IM0467M01
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AZ65686 IM055G10
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AZ64786 IM055G10
AZ64786 IM0563G19
AZ64781 IM0513018
AZ64881 ZM0218A01
AZ64881 ZM0218A02
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AZ990856 ZM0274F14
AB088508 AB088508
BQ593049 E012375-0
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AZ359199 1M0101M19
AZ369273 1M0119H13
AZ387347 1M0146K12
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5009-0-42-D11.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 14)
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E., Frankel
J. and Klobutcher, L.
BST from Terrahymena thermophila, strain CU428.1, growing cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tetrahymena thermophila
Eukaryota, Alveolata, Ciliophora, Oligohymenophorea,
Hymenostomatida, Tetrahymenina, Tetrahymena.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
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AAA771151
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BM398220.1 GI:18198273
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   BM398220 5009-0-42
AI424037 tf51h06.x
AI685758 tu37g09.x
AI721735 fc31g08.x
                                                                  December 31, 2003, 13:58:09; Search time 574.494 Seconds (without alignments) 211.530 Million cell updates/sec
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          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Gapop 10.0, uapear ...

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Animum DB seq length: 0

Maximum DB seq length: 30

Geot-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                             /db_xref="taxon:5911"
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preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
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/lab host="DH10B"
organism="Tetrahymena thermophila"
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Seg primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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Homo sapiens
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05/19/2004

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/iou_lib="NIIO"
//clone_lib="NIIO"
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//clone_lib="NIIO"
//note="Organ: prostate; Vector: pT773D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI CGAP Pr22 was prepared, and ss
circles were made in vItro. Following HAP purification,
this DNA was used as tracer in a subtractive hypridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
985608-986759, 1101192-1101959, and 121728-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
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Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDN Library Preparation: M. Bento Soares, Ph.D.
CDN Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Mashington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Length 16;
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100.0%; Score 5; DB 9; Le 100.0%; Pred. No. 1.8e+06;
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Seg primer: -400P from Gibco
High quality sequence scop: 1.
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Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J., Sathe, G., Mui, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Onz.comithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay_kumar-1@gsk.com
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HNC11-1-G8.R HNC (Human Normal Cartilage) Homo sapiens CDNA, mRNA
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                                                  Gaps
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UW2109
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Homo sapiens
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Matches 5; Conservative
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Unter_ESTs: fc31908.y1

Contact: Stephen L. Johnson

Washington University School of Medicine

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Fax: 316 286 1800

Fax: 3
                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                 i (bases 1 to 16)

Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, S., Hillier, L., Theishag, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
                        EST 07-JUN-2001
16 bp mRNA linear EST 07-JUN-200: EG11g08.X1 Zebrafish WashU MPIMG EST Danio rerio cDNA clone IMAGE:3723038 3' similar to SW:YM14_PARTE P15615 HYPOTHETICAL 47.2 A1731715.
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stage_embryos"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seg primer: T7 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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    .16
    /organism="Danio rerio"

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/db_xref="taxon:7955"
/clone="IMAGE:3723038"
                                                                                                                                                                                     Danio rerio (zebrafish)
                                                                                                                 AI721735
AI721735.1 GI:5040064
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                                                                                                                                                                                                          Danio rerio
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05719/2004
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/tissue type="developing root"
/lab_host="EMDH10B"
/clone lib="MPIZ-ADIS-024-developing root"
/note="Vector: pGWVSPORT6; Site_1: Sall; Site_2: Not1;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sall-Not1, primer sites and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing granted in the context of the GABI-Beet project , local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
                                "mol type="mRNA"
'cultivar="KWS2320 (double haploid, monogerm breeding line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C21103 17 bp mRNA linear EST 31-DEC-2002 HUMGS0002626 Human adult (K.Okubo) Homo sapiens cDNA 3', mRNA
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SP6-Sall-CCACGCGTCCG-5prime-cDNA-polyA-CC-Not1-T7; Note:
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 17)
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Institute for Molecular and Cellular Biol
Osaka University
1-3, Yamada-oka, Suita, Osaka Pref. 565, Japan
1-3, Kamada-oka, Suita, Osaka Pref. 565, Japan
Tel: 66-877-511(ex.3315)
Email: kousaku@imcb.osaka-u.ac.jp
We are not submitting the same cDNA sequence redundantly to DDBJ
Since 1993. For the abundance information of clones with this sequence in this library and as well as in other 3'-directed libraries, see 'http://www.imcb.osaka-u.ac.jp/bodymap'. The sequences of the clones represented by this GS sequences is also found there.
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/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_ge="adult"
/clone_lib="Human adult (K.Okubo)"
/note="One or more human adult tissue"
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      organism="Beta vulgaris"
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/db_xref="taxon:161934"
/clone="024-022-H17"
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Contact: Weisshaar B MPIZ
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research Carl-von-Linne Weg 10, 50829 Koeln, Germany Fax: 00492215062851

Email: weisshaa@mpiz-koeln.mpg.de Insert Length: 17 Std Error: 0.00
Plate: 22 row: H column: 17
Seq primer: SP6; CATAGGATTAGGGGACACTATAG.
Location/Qualifiers
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 17)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
and Radelof,U.
                                                                                             Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J.,
Sathe, G., Mui, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                              GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/db_xref="taxon:9606"
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/lab host="E.coli DH0 B"
/note="vector: pSPORT I; Site_1: SalI; Site_2: NotI;
Directional"
                                                                                                                                                                                       Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage CDNA libraries osteoarthr. Cartil. 9 (7), 641-653 (2001)
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lmer: T7.
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EST.
                                                                                                                                                                                                                                                                                                                                                                                 Contact: Sanjay Kumar
                                                                   (bases 1 to 17)
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Email: sanjay kume
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Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
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Best Local Similarity 100.
Matches 5; Conservative
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AI120725/c
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                                                                                                                                                                                                                                       EST 17-JAN-2002
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/db_xref="taxon:5911"
/clone lib="chicoat/Turkewitz cDNA (large fraction)"
/clone lib="chicoat/Turkewitz SK+; Details on library
/note="Vector: BlueScript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
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Turkewitz, A.P., Varrer, K.M., Jahn, C., Orias, E., Kirk, K.E., Frankel
J. and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 19)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
        Gaps
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18437954.1 Criston
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Eukaryota, Alveolata, Ciliophora, Oligohymenophorea,
Hymenostomatida, Tetrahymenina, Tetrahymena.
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     0; Indels
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Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
  0; Mismatches
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Email: apturkew@midway.uchicago.edu
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Email: cgapbs-r@mail.nih.gov
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/strain="CU428.1"
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Homo sapiens
  5; Conservative
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Unpublished
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Best Local Similarity
Matches 5; Conserv
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/clone="IMAGE:1587278"
/tissue_type="pooled germ cell tumors"
/tissue_type="pooled germ cell tumors"
/tissue_type="Dooled germ cell tumors"
/clone lib="WICI CGAP GC4"
/note="Vector: pT7135-pac (Pharmacia) with a modified
polylinker; lst strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT713
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo. "
Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NT-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mamala; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 19)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HHMI Mouse EST Project
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ub72b11.rl Soares_mammary_gland_NMLMG Mus musculus cDNA clone
IMAGE:1383261 5' similar to TR:QIS009 QIS009 ORF, COMPLETE CDS. ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone is available royalty-free through LLNL , contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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Tel: 314 286 1800
Fax: 314 286 1810
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WashU-HHMI Mouse EST Project
Washington University School of MedicineP
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Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/clone_lib=androm mouse embryo mewa"
/clone_lib=androm mouse embryo mewa"
/note=Tvetcs: pME18S-FL3; Site_1: DraIII (CACTGTGTG);
Site_2: DraIII (CACCATGTG); lst Strand cDNA was primed
with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTTT];
double-stranded cDNA was ligated to a DraIII adaptor
[TGTTGGCCTACTGG], digested and cloned into distinct DraIII
sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site
CACCATGTG). XhoI should be used to isolate the cDNA
insert. Size selection was performed to exclude fragments
cl.5kb. Library constructed by Dr. Sumio Sugano
(University of Tokyo Institute of Medical Science).
Custom primers for sequencing: 5' end primer
CGACTGGAGCTGGAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C00646 19 bp mRNA linear EST 31-DEC-2002 HUMGS0008192 Human adult (K.Okubo) Homo sapiens cDNA, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 19)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1-3) Yamada-oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-5111(ex.3315)
Tel: 06-877-5111(ex.3315)
We are not submitting the same cDNA sequence redundantly to DDBJ since 1993. For the abundance information of clones with this sequence in this library and as well as in other 3 -directed libraries, see 'http://www.imcb.osaka- u.ac.jp/bodymap/. The sequences of the clones represented by this GS sequences is also
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/organism="Homo sapiens"

/organism="mRNA"

/db_xref="mRNA"

/db_xref="tage="adult"

/dev_srage="adult"

/clone lib="Human adult (K.Okubo)"

/note="One or more human adult tissue"

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Institute for Molecular and Cellular Biol
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t
                   /dev_stage="embryo, 14 dpc"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
/clone="IMAGE:2088249"
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Best Local Similarity 100...
5, Conservative
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5; Conservative
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                                                                                                                                                                                                                                                 /clone_lib="Soares mammary gland_NMLMG"
/note="Vector: py773D-Pac (Pharmacia) with a modified
polylinker; lst strand cDNA was prepared from mammary
gland tissue from a lactating female, and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified py773 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo. "
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Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, E., Swaller, T., Gibbons, M., Pape, D., Harvey, M., Schurk, R., Ritter, F., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Ritter Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AI747751 1 sugano mouse embryo mewa Mus musculus cDNA clone IMAGE:2088249 3' similar to TR:P79101 P79101 CLEAVAGE AND POLYADENYLATION SPECIFITY FACTOR PROTEIN: ;, mRNA sequence. AI747751
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on wrong strand
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Contact: Marra M/WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 5; DB 9; Le
100.0%; Pred. No. 1.9e+06;
                 Seg primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 1. Location/Qualifiers
                                                                                                                                                                                     /sex="female (lactating)"
/tissue_type="mammary gland"
/lab_host="DH10B"
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reversed clone: similarity
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                                                                                                        organism="Mus musculus"
                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:10090"
                                                                                                                                                                    clone="IMAGE:1383261"
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High quality sequence stop: 1
Location/Qualifiers
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/strain="C57BL"
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Gaps

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Gaps

us-09-540-843-4.szlm30.rst

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/sex="Male" coll strain X110-Gold, T1-resistant, F-"
/lab host="E. Coli strain X110-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
/(http://www.jax.org/resources/documents/dnares/). The DNA
was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil 4732114] gbl AFL29072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Punn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                AZ345849 108S 29-SEP-200 1900080D16R Mouse 108b plasmid UUGCIM library Mus musculus genomic clone UUGCIM0080D16 R, genomic survey sequence.
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Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: D column: 16
Seq primer: CACACAGGAAAACAGCTAATGACC
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University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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/clone="UUGC1M0080D16"
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Location/Qualifiers
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Mus musculus
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longarer, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R., Pouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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19 bp DNA linear GSS 29-SEP-200
1M0074004R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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/clome_lib="Mouse 10kb plasmid UNGCIM library"
/note="Wector: PWD4Zuv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0074 row: O column: 04
Seq primer: CACACAGGAAACAGCTAATGACC
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/strain="C57BL/6J"
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/clone="UUGC1M0074004"
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Location/Qualifiers
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Oy 1 GTATG 5 ||||| | Db 13 GTATG 9 Search completed: December 31, 2003, 19:41:20 Job time : 578.494 secs

Copied from 09980559 on 05/19/2004

Perfect score:

Run on:

Sequence:

Scoring table:

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Sequence 11, Appl
Sequence 11, Appl
Sequence 223, App
Sequence 2256, Ap
Sequence 2226, Ap
Sequence 2220, Ap
Sequence 2220, Ap
Sequence 2220, Ap
Sequence 2256, Ap
Sequence 2256, Ap
Sequence 1256, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 13, Appl
Sequence 622, Appl
Sequence 632, Appl
Sequence 636, Appl
Sequence 636, Appl
Sequence 1341, Appl
Sequence 1343, Appl
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Sequence 636, App
Sequence 1338, Ap
  Sequence 224,
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| Publication No US20030032610A1
| GENERAL INPORMATION:
| APPLICANT: Glichreet, Barbara A. |
| APPLICANT: Glichreet, Barbara A. |
| APPLICANT: Glichreet, Barbara A. |
| APPLICANT: Slich Mark S. |
| TITLE OF INVENTION: Method to Inhibit Cell Growth Using TITLE OF INVENTION: Method to Inhibit Cell Growth Using FILE REFERENCE: 0054.1080-108 |
| CURRENT APPLICATION NUMBER: US 08/467,012 |
| PRIOR FILING DATE: 1995-06-06 |
| PRIOR FILING DATE: 1996-06-03 |
| PRIOR FILING DATE: 1996-06-03 |
| PRIOR FILING DATE: 1996-03-31 |
| PRIOR FILING DATE: 2000-03-31 |
| PRIOR FI
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US-09-990-186-6231
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US-09-999-994-623
US-09-999-994-623
US-09-999-994-2256
US-09-999-994-2256
US-10-122-630-1
US-10-122-630-1
US-10-122-630-1
US-09-989-789-622
US-09-989-789-622
US-09-989-789-622
US-09-989-789-622
US-09-989-789-622
US-09-989-789-622
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US-09-989-789-1338
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US-09-962-602-8
US-09-990-186-622
US-09-990-186-632
US-09-990-186-1338
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  Query Match
Best Local Similarity 100.
Matches 5; Conservative
1 GTATG 5
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Sequence 178029,
Sequence 178029,
Sequence 178029,
Sequence 178021,
Sequence 178021,
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Sequence 17, Appl
Sequence 6, Appli
                                                                                                                                                                                 December 31, 2003, 17:10:00 ; Search time 58.2911 Seconds (without alignments) 296.896 Million cell updates/sec
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Sequence 6, P
Sequence 4, P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Ggn2_6'ptodata/1/pubpna/USO7_PUBCOMB. seq:*
'Cgn2_6'ptodata/1/pubpna/PCT_NEW_PUB. seq:*
'Cgn2_6'ptodata/1/pubpna/USO6_NEW_PUB. seq:*
'Cgn2_6'ptodata/1/pubpna/USO6_PUBCOMB. seq:*
'Cgn2_6'ptodata/1/pubpna/USO6_PUBCOMB. seq:*
'Cgn2_6'ptodata/1/pubpna/PCTUB_PUBCOMB. seq:*
'Cgn2_6'ptodata/1/pubpna/USO8_NEW_PUB. seq:*
'Cgn2_6'ptodata/1/pubpna/USO8_PUBCOMB. seq:*
'Cgn2_6'ptodata/1/pubpna/USO8_PUBCOMB. seq:*
'Cgn2_6'ptodata/1/pubpna/USO9_PUBCOMB. seq:*
'Cgn2_6'ptodata/1/pubpna/USO9_NEW_PUB. seq:*
'Cgn2_6'ptodata/1/pubpna/USO0_NEW_PUB. seq:*
'Cgn2_6'ptodata/1/pubpna/USO0_NEW_PUB. seq:*
'Cgn2_6'ptodata/1/pubpna/USO0_NEW_PUB. seq:*
'Cgn2_6'ptodata/1/pubpna/USO0_NEW_PUB. seq:*
'Cgn2_6'ptodata/1/pubpna/USO0_NEW_PUB. seq:*
'Cgn2_6'ptodata/1/pubpna/USO0_NEW_PUB. seq:*
'Cgn2_6'ptodata/1/pubpna/USO0_PUBCOMB. seq:*
'Cgn2_6'ptodata/1/pubpna/USO0_PUBCOMB. seq:*
                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-122-630-6
US-10-122-633-6
US-10-122-633-6
US-10-122-633-6
US-10-027-632-178029
US-10-027-632-178029
US-10-027-632-178029
US-10-122-630-3
US-10-122-633-3
US-10-122-633-3
US-10-122-633-7
US-09-927-886-17
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gapop 10.0 , Gapext 1.0
Searched: 2263443 seqs, 1730637950 residues
Animum DB seq length: 0
Faximum DB seq length: 30
Post-processing: Minimum Match 0$
Maximum Maximum Match 100
Fight of Commercian 15 of Commer
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: POlymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2000-04-30
PRIOR PELING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR PILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-09-28
                                                                                                                                                                                                                                          Sequence 6, Application US/10122633
| Publication No US20030032611A1
| GENERAL INFORMATION:
| APPLICANT: Glichrest, Barbara A.
| APPLICANT: Eller, Mark S.
| APPLICANT: Taar, Mina
| TITLE OF INVENTION: Method to Inhibit Cell Growth Using
| TITLE OF INVENTION: Method to Inhibit Cell Growth Using
| TITLE OF INVENTION: Method to Inhibit Cell Growth Using
| TITLE OF INVENTION: Oligonucleotides
| CURRENT APPLICATION WINBER: US 99/540,843
| PRIOR APPLICATION NUMBER: PCT/US01/10162
| PRIOR APPLICATION NUMBER: PCT/US01/10162
| SOFTWARE: PastSEQ for Windows Version 4.0
| SEQ ID NO 6
| SEQ ID NO 6
Query Match 100.0%; Score 5; DB 15; Length 5; Best Local Similarity 100.0%; Pred. No. 6.7e+08; Matches 5; Conservative 0; Mismatches 0; Indels
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100.0%; Score 5; DB 15; I
Best Local Similarity 100.0%; Pred. No. 6.7e+08;
Matches 5; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Synthetic DNA Fragment
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NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 178029, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-027-632-178029/c
                                                                                            1 GTATG 5
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                                                                                                                             Length 5;
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                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/122,630
CURRENT FILING DATE: 2002-04-12
PRIOR PELICATION NUMBER: US 08/467,012
PRIOR FILING DATE: 1995-06-06
PRIOR FILING DATE: 1996-06-03
PRIOR PILING DATE: 1996-06-03
PRIOR PILING DATE: 1996-03-26
PRIOR PILING DATE: 1998-03-26
PRIOR PILING DATE: 1998-03-36
PRIOR FILING DATE: 1998-03-36
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 6
ENGTH: 5
TYPE: DNA
CRGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic DNA Fragment
COTHER INFORMATION: Synthetic DNA Fragment
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Matches 5; Conserv
                       1 GTATG S
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us-09-540-843-4.szlm30.rnpb

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GENERAL ILLY CARALTON:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
ITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REPERENCE: 108927.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2002-04-30

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR PLICATION NUMBER: US 60/183,483

PRIOR PLICATION NUMBER: US 60/185,218

PRIOR PLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 1900-02-24

PRIOR FILING DATE: 1900-09-28

PRIOR PLICATION NUMBER: US 60/167,363

PRIOR PLICATION NUMBER: US 60/166,363

PRIOR PLICATION NUMBER: US 60/146,002

PRIOR PLING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-08

NUMBER OF SEQ ID NOS: 325720

SOOTWARE: Fastere for Windows Version 4.0
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4.8e+08;
                   PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR PELICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-028
PRIOR FILING DATE: 1999-09 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SSOTANARE: FastSEQ for Windows Version 4.0
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100.0%; Score 5;
Best Local Similarity 100.0%; Pred. No.
Matches 5; Conservative 0; Mismatci
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; Sequence 178043, Application US/10027632
; GENERAL INFORMATION:
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Publication No. US20030032610A1
GENERAL INFORMATION:
APPLICANT: Gilchrest, Barbara A.
APPLICANT: Biler, Mark S.
APPLICANT: Yaar, Mina
     FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Conservative
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Best Local Similarity
Matches 5; Conserv
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US-10-027-632-178029
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GENERAL INFORMATION:
JAPLICANT WARG, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT PILING DATE: 2002-04-30
FRIOR FILING DATE: 2000-07-12
FRIOR FILING DATE: 2000-07-12
FRIOR PAPLICATION NUMBER: US 60/198,676
FRIOR FILING DATE: 2000-04-20
FRIOR FILING DATE: 2000-07-20
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Polymorphisms in the Human Genome FILE REFERENCE: 108927.129
FULE REFERENCE: 108927.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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                                                                                                                              100.0%; Score 5; DB 13; Length 7; 100.0%; Pred. No. 4.8e+08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-08
SOFTWARE: FRESEQ FOR WINGOWS Version 4.0
SOFTWARE: FRESEQ FOR WINGOWS Version 4.0
                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 178043, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
                                                                                                  Query Match
Best Local Similarity luv...
5; Conservative
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ORGANISM: Human

OBENIO-027-632-178043

Ouery Match

Best Local Similarity

Matches 5; Conservat
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                                                                                                                                                                                                                                      1 GTATG 5
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                        ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178029
LENGTH: 7
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APPLICANT: Gilchrest, Barbara A.

APPLICANT: Gilchrest, Mark S.

APPLICANT: Bilchr, Mark S.

TITLE OF INVENTION: Method to Inhibit Cell Growth Using
TITLE OF INVENTION: Oligonucleotides

TITLE OF INVENTION: Oligonucleotides

TITLE TEREBERENCE: 0054.1088-019

CURRENT APPLICATION NUMBER: US/10/12,633

CURRENT APPLICATION NUMBER: US/09/540,843

PRIOR APPLICATION NUMBER: PCT/US01/10162

PRIOR APPLICATION NUMBER: PCT/US01/10162

PRIOR PELING DATE: 2001-03-30

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastsEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                          | GENERAL INCRMATION: | JAPPLICANT: Glichrest, Barbara A. |
| APPLICANT: Glichrest, Mark S. |
| APPLICANT: Eller, Mark S. |
| APPLICANT: Eller, Mark S. |
| APPLICANT: Yaar, Mina |
| TITLE OF INVENTION: Method to Inhibit Cell Growth Using |
| TITLE OF INVENTION: Oligonucleotides |
| FILE REFERENCE: 0004-1086-109 |
| CURRENT PILING DATE: 2002-04-12 |
| PRIOR APPLICATION NUMBER: US 09/540,843 |
| PRIOR APPLICATION NUMBER: PCT/US01/10162 |
| PRIOR APPLICATION NUMBER: PCT/US01/10162 |
| PRIOR APPLICATION NUMBER: PCT/US01/10162 |
| PRIOR PILING DATE: 2001-03-30 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
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100.0%; Pred. No. 4.8e+08;
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100.0%; Pred. No. 4.8e+08;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , OTHER INFORMATION: Synthetic DNA Fragment US-10-122-633-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-7
                                                                                                                                                                                                                      Sequence 3, Application US/10122633 Publication No. US20030032611A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-122-633-7
; Sequence 7, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Goet Local Similarity 100.v.
Best Local Si Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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                 2 GTATG 6
                                                                                                                                                                                           US-10-122-633-3
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SEQUENTARE: FASTOLE.

TYPE: DNA

ORGANISM: Artificial Sequence
FRATURE:
OTHER INFORMATION: Synthetic DNA Fragment

OTHER INFORMATION
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Cosquence 7, Application US/10122630

Publication No. US2030032610A1

GENERAL INFORMATION:

APPLICANT: Gilchrest, Barbara A.

APPLICANT: Biler, Mark S.

APPLICANT: Biler, Mark S.

TITLE OF INVENTION: Oligomotelectides

CURRENT APPLICATION NUMBER: US/10/122,630

CURRENT FILING DATE: 1995-06-06

PRIOR APPLICATION NUMBER: US 08/467,012

PRIOR PILING DATE: 1996-06-03

PRIOR PILING DATE: 1996-06-03

PRIOR PILING DATE: 1998-03-26

PRIOR PILING DATE: 2000-03-31

PRIOR PILING DATE: 2000-03-31

PRIOR APPLICATION NUMBER: PCT/US01/10162

PRIOR APPLICATION NUMBER: PCT/US01/10162

PRIOR APPLICATION NUMBER: PCT/US01/10162

PRIOR PILING DATE: 2000-03-31

PRIOR APPLICATION NUMBER: PCT/US01/10162

PRIOR PILING DATE: 2001-03-30

PRIOR PILING DATE: 2001-03-30

NUMBER OF SEQ ID NOS: 15

SEQUENCE: PARCENT APPLICATION NUMBER: PCT/US01/10162

PRIOR PILING DATE: 2001-03-30

NUMBER OF SEQ ID NOS: 15

PRIOR PLING DATE: 2001-03-30

PRIOR PILING DATE: 2001-03-30

PRIOR PILING DATE: 2001-03-31

PRIOR PILING DATE: 2001-03-31
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TITLE OF INVENTION: Method to Inhibit Cell Growth Using TITLE OF INVENTION: Oligonucleotides FILE REPERBRACE: 0054.1088-018
CURRENT APPLICATION NUMBER: US/10/122,630
CURRENT APPLICATION NUMBER: US/467,012
PRIOR APPLICATION NUMBER: US 08/467,012
PRIOR PILING DATE: 1995-06-06
PRIOR PILING DATE: 1995-06-03
PRIOR PILING DATE: 1996-06-03
PRIOR PILING DATE: 1996-06-03
PRIOR PILING DATE: 1998-03-13
PRIOR PILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
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US-10-122-630-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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2 GTATG 6
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2 GTATG 6

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1 GTATG 5

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us-09-540-843-4.szlm30.rnpb

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Sequence 6, Application US/09861014

| Sequence 6, Application US/09861014
| Patent No. US20020115216A1
| GENERAL INFORMATION:
| APPLICANT: Steer, Clifford
| APPLICANT: McIver, Betsy
| APPLICANT: Hackett, Perry
| APPLICANT: Hackett, Perry
| APPLICANT: Hackett, Perry
| APPLICANT: McIver, R.
| FILE REFERENCE: 110.01330101
| CURRENT FILING DATE: 2001-05-19
| PRIOR FILING DATE: 2000-05-19
| PRIOR FILING DATE: 2001-04-20
| NUMBER OF SEQ ID NOS: 10
| SOFTWARE: PatentIn version 3.0
| SEQ ID NO 6
| LENGTH: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 8;
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                                                                                                                                                                                                                                                                                OTHER INFORMATION: transposon repeat sequence
                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
          CURRENT APPLICATION NUMBER: US/09/927,886
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/162,279
PRIOR PILING DATE: 1999-10-28
FRIOR APPLICATION NUMBER: 09/440,301
PRIOR FILING DATE: 1999-11-17
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Direct repeat sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: January 1, 2004, 01:10:36 Job time : 58.2911 secs
                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
FILE REFERENCE: STAN-160CIP
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity luv.
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Best Local Similarity 100.
Matches 5; Conservative
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US-09-861-014-6/c
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                                                                   Sequence 11, Application US/09142593

Sequence 11, Application US/09142593

Sequence 11, Application US/09142593

GENERAL INFORMATION:

APPLICANT: HACKETT ET AL.

TITLE OF INVENTION: INTRODUCTION OF NUCLEIC ACID INTO DNA OF A CELL.

NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESS:

ADDRESSE: MUETING, RAASCH & GEBHARDT, P.A.

STREET: 119 NORTH FOURTH STREET, SUITE 203

CITY: MINNEAPOLIS

STATE: MINNEAPOLIS

STATE: MINNESOTA

COUNTRY: USA

ZIP: 55402

COMPUTER READBALE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IP-DOPY disk

COMPUTER: PRE-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/142,593

FILING DATE: 10-SEP-1998

PILING DATE: 10-SEP-1998
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APPLICANT: Yant, Stephen
TITLE OF INVENTION: Methods of In Vivo Gene Transfer Using a
TITLE OF INVENTION: Sleeping Beauty Transposon System
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 9; Length 8; 4.2e+08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: SANDBERG, VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 110.00450101
TELECOMUNICATION INFORMATION:
TELEPHONE: 612-305-1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/040,664
FILING DATE: 11-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/053,868
FILING DATE: 28-JUL-1997
APPLICATION NUMBER: 60/065,303
FILING DATE: 13-NOV-1997
PRIOR APPLICATION NUMBER: 60/065,303
FILING DATE: 13-NOV-1997
PRIOR APPLICATION NUMBER: 90/065,303
FILING DATE: 11-MAR-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 5; 100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 5; Conserv
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GTATG 2
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US-09-927-886-17/c
                                                      US-09-142-593-11/c
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                                                                                        December 31, 2003, 11:36:21 ; Search time 1012.7 Seconds (without alignments) 444.364 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Gapop 10.0, Gapext 1.0

Gapop 10.0, Gapext 1.0

Gapop 10.0, Gapext 1.0

Minimum DB seq length: 0

Maximum DB seq length: 30

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Pred. No. is the number of results predicted by chance to have a

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

C 1 11 100. 0 11 6 AR026486 AR026496 Sequence C 2 3 11 100. 0 11 6 AR026489 AR026496 Sequence C 3 11 100. 0 11 6 AR026489 AR026496 Sequence C 3 11 100. 0 11 6 AR026499 AR026495 Sequence C 5 11 100. 0 11 6 AR026495 AR026495 Sequence C 5 11 100. 0 11 6 AR026495 AR026495 Sequence C 10 11 100. 0 11 6 AR026495 AR026495 Sequence C 10 11 100. 0 11 6 AR026495 AR026495 Sequence C 10 11 100. 0 11 6 AR026495 AR026495 Sequence C 10 11 100. 0 11 6 AR026495 AR026495 Sequence C 10 11 100. 0 11 6 AR026495 AR026495 Sequence C 10 11 100. 0 11 6 BD071064 BD071077 Modulation C 12 11 100. 0 11 6 BD071064 BD071064 MODULation C 12 11 100. 0 11 6 BD071064 BD071064 MODULation C 12 11 100. 0 11 6 BD071064 BD071064 MODULation C 12 11 100. 0 11 6 BD071064 BD071064 BD071064 MODULation C 12 11 100. 0 11 6 BD071064	Re	Result No. So	core	Query Match I	Length	DB	ΩI		Descri	ript	ion	
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11   1000   11   6 AR059195   A	t		1:	100.0	7 ;	ט ס	AKU26486		ARU	00407	Sequence	
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11   100.0   11   6   AR161904   AR161904   AR161904   AR161904   AR268751   AR26875	י נ		; ;	0.00	1:	ט ע	AP075506		COCK	15506	Semience	
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1 (bases 1 to 11)
Villeponteau, B., Feng, J., Funk, W. and Andrews, W.H. Mammalian telomerase
Patent: US 6258535-A 2 10-JUL-2001;
                                                                                                                                               Villeponteau, B., Feng, J., Funk, W. and Andrews, W.H. Mammalian telomerase
Patent: US 5837857-A 2 17-NOV-1998;
Location/Qualifiers
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Villeponteau, B., Feng, J., Funk, W. and Andrews, W.H.
Wammallian telomerase
Patent: US 5958680-A 3 28-SEP-1999;
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Sequence 2 from patent US 6258535.
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Windle, B.E., Qiu, M., Chen, S.-F., Fletcher, T.M. and Maine, I.
Rapid and sensitive assays for detecting and distinguishing between
processive and non-processive telomerase activities
Patent: us 5856056-A 11 05-JAN-1999;
Location/Qualifiers
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Windle, B.E., Qiu, M., Chen, S.-F., Fletcher, T.M. and Maine, I.
Rapid and sensitive assays for detecting and distinguishing between
processive and non-processive telomerase activities
Patent: US 5856096-A 12 05-0AN-1999;
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/organism="synthetic construct"
/mol_type="genomic DNA"
/mol_type="genomic SA63"
/db xref="texcn:32630"
/note="Synthetic DNA Fragment"
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/organism="synthetic construct"
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/mol_type="genomic DNA"
/db xref="taxon:32630"
/note="Synthetic DNA Fragment"
/ a S C 0 g 2 t
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Sequence 5 from Patent WO0174342.
AX268757
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Villeponteau, B., Feng, J., Funk, W. and Andrews, W.H. Mammal.ian telomerase
Patent: US 6548298-A 2 15-APR-2003;
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Patent: WO 0046601-A 10-AUG-2000;
LARSEN FRANK (NO) ; SKAANSENG MARIANNE (NO)
LOCATION/Qualifiers
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Sequence 2 from patent US 6548298.
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Sequence 5 from Patent WO0046601.
AX033373 GI:10280147
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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Location/Qualifiers
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linear PAT 20-NOV-2001

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אסטיביער PAT 27-AUG-2002 אסטיבונים of mammalian telomerase by peptide nucleic acids.
BD071077
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Strandedness: Single;
Topology: Linear;
/desc = 'peptide nucleic acid (PNA), where (deoxy(ribose- CC
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JP 2001517929-A/30
09-007-2001
09-007-2010
09-APR-1997 UP 1997536487
09-APR-1996 US 08/630019
JERRY W SHAY, WOODRING E WRIGHT, MIECZYSLAW A PIATYSZEK, DAVID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unclassified.

1 (bases 1 to 11)
Shay,J.W., Wright,W.E., Piatyszek,M.A., Corey,D. and Norton,J.C.
Modulation of mammalian telomerase by peptide nucleic acids
Patent: JP 2001517929-A 30 09-OCT-2001;
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100.0%; Pred. No. 3.7e+04;
iive 0; Mismatches 0;
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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JP 2001517929-A/43.
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JP 2001517929-A/30.
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Shay,J.W., Wright,W.E., Piatyszek,M.A., Corey,D. and Norton,J.C. Modulation of mammalian telomerase by peptide nucleic acids Patent: JP 2001517929-A 13 09-OCT-2001;
GERON CORP.
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/organism="synthetic DNA"
/db_xref="taxon:12630"
/note="Beschreibung der kuenstlichen Sequenz:
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Strandedness: Single;
Topology: Linear;
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Sequence 60 from Patent WO0179249.
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JP 2001517329-A/13
09-00T-2010
09-ARR-1997 JP 1997536487
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JP 2001517929-A/13.
unidentified
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               1 (Dases 1 to 11.0)

Shay, J.W., Wright, W.B., Piatyszek, M.A., Corey, D. and Norton, J.C.
Modulation of mammalian telomerase by peptide nucleic acids
Batent: JP 2001517929-A 43 09-OCT-2001;
GERON CORP
OS Unidentified
N JP 2001517929-A/43
PD 09-OCT-2001
PP 09-OFT-2001
PP 09-APR-1997 JP 1997536487
PR 09-APR-1996 US 08/630019
PP JERRY W SHAY, WOODRING E WRIGHT, MIECZYSLAW A PIATYSZEK, DAVID
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1 (bases 1 to 11)
Villeponteau, B., Feng, J., Funk, W. and Andrews, W.H. Mammalian telomerase
Patent: JP 2002272489-A 2 24-SEP-2002;
GERON CORP
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Strandedness: Single;
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Adeso: - 'phosphorothioate (PS) nucleic acid'
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Location/Qualifiers
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/organism='Unidentified'
Location/Qualifiers
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

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    /organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"

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Mammalian telomerase.
BD176143
BD176143.1 GI:29121847
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JAMES C NORTON
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       (bases 1 to 11)
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		N3 to P5 oligonucl	DNA oligonucleotid	Peptide nucleic ac	Telomerase primer.	PNA sequence #13 u	PNA sequence #18 u	PNA sequence #19 u	PNA sequence #31 u
SUMMARIES	<u> </u>		AAV07769	AAT89250	AAT89237	AAT90060	AAA37556	AAA37561	AAA37562	AAA37573
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40 11 100.0 13 25 AB58497 Tel 41 11 100.0 15 18 AAT99226 Pep 42 11 100.0 15 18 AAT99299 Pep 43 11 100.0 15 18 AAT90068 Tel 44 11 100.0 15 21 AAA7545 PNA 45 11 100.0 15 21 AAA37548 PNA ALIGNMENTS	40 11 100.0 13 25 AB558497 Tel 41 11 100.0 15 18 AAT89226 Pep 42 11 100.0 15 18 AAT89229 Pep 43 11 100.0 15 18 AAT9068 Tel 44 11 100.0 15 21 AAA37545 PNA 45 11 100.0 15 21 AAA37548 PNA ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS		11	100.	13	23	ABF02803	Oligonucleotide SE
41 11 100.0 15 18 AAT89226 Peptide nucleic a 42 11 100.0 15 18 AAT89229 Peptide nucleic a 43 11 100.0 15 18 AAT89068 Telomerase priner 44 11 100.0 15 21 AAA37545 PNA sequence #2 u 45 11 100.0 15 21 AAA37548 PNA sequence #5 u AAA37548 ALIGNMENTS	41 11 100.0 15 18 AATB9226 Peptide nucleic a 42 11 100.0 15 18 AATB9229 Peptide nucleic a 43 11 100.0 15 18 AAT90068 Telomerase primer 44 11 100.0 15 21 AAA7545 PNA sequence #2 u 45 11 100.0 15 21 AAA37548 PNA sequence #5 u 50.0 15 21 AAA37548 PNA sequence #5 u 50.0 15 21 AAA37548 PNA sequence #5 u AAV07769 standard; DNA; 11 BP.	40	11	100.	13	25	9	Telomerase inhibit
42 11 100.0 15 18 AAT99229 Peptide nucleic a 11 100.0 15 18 AAT990068 Telomerase primer 44 11 100.0 15 21 AAA37545 PNA sequence #2 u 45 11 100.0 15 21 AAA37548 PNA sequence #5 u AAIGNMENTS	42 11 100.0 15 18 AAT99229 Peptide nucleic a 43 11 100.0 15 18 AAT9068 Telomerase primer 44 11 100.0 15 13 AAA7945 PNA sequence #2 u 45 11 100.0 15 21 AAA37548 PNA sequence #2 u 45 11 100.0 15 21 AAA37548 PNA sequence #5 u 20 AAA7769 Standard; DNA; 11 BP.	41	11	100.	15	18	AAT89226	g G
43 11 100.0 15 18 AAT90068 Telomerase primer 44 11 100.0 15 21 AAA37545 PNA Sequence #2 u 45 11 100.0 15 21 AAA37548 PNA Sequence #5 u ALIGNMENTS	43 11 100.0 15 18 AAT90068 Telomerase primer 44 11 100.0 15 21 AAA37545 PNA sequence #2 ud 45 11 100.0 15 21 AAA37548 PNA sequence #5 ud 707769 AAV07769 Standard; DNA; 11 BP.	42	ij	100.	15	18	AAT89229	
11 100.0 15 21 AAA3'545 PNA sequence #2 ui 11 100.0 15 21 AAA3'7548 PNA sequence #5 ui ALIGNMENTS	44 11 100.0 15 21 AAA37545 PNA sequence #2 us 45 11 100.0 15 21 AAA37548 PNA sequence #5 us 11 100.0 15 21 AAA37548 PNA sequence #5 us 2ULT 1 SULT 1 AAV07769 AAV07769 standard; DNA; 11 BP.		11	100.	12	18	9	Telomerase primer
11 100.0 15 21 AAA37548 PNA sequence #5 u	45 11 100.0 15 21 AAA37548 PNA sequence #5 uu ALIGNMENTS 507769 AAV07769 standard; DNA; 11 BP.	44	11	٥.	15	21	4	
ALIGNMENTS	UULT 1 707769 AAV07769 standard; DNA; 11 BP.	45	11		15	21	754	sednence #5 n
	SULT 1 707769 AAV07769 standard; DNA; 11 aav07769.						ALIGNMENTS	
	AAV07/69 Standard; DNA; 11	300	1					
50LT 1 707769				standard;	DNA;			
50LT 1 707769 AAV07769 standard; DNA; 11			V07769.					

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N3 to P5 oligonucleotide phosphoramidate useful as telomerase inhibitor.
                                               telomerase inhibitor; phosphoramidate; telomerase-binding region; TBR; cell proliferation; tumour; lukaemia; duplex; ss.
                                                                                                               /*tag= a
/note= "each linkage is a phosphoramidate linkage"
                                                                                              Location/Qualifiers
                                                                                                                                                                                                    96US-0630242.
                                                                                                                                                                                 97WO-US05773.
          07-DEC-1998 (first entry)
                                                                                                                                                                                08-APR-1997;
                                                                                                                                            WO9737691-A1
                                                                                                                                                                                                    10-APR-1996;
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telomerase, and include the sequence GGG for specific

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mammalian
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AAT89237
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                                                                                                                                                                                                                                                                                                                           The invention relates to treatment of conditions associated with high administering an oligonucleotide N3' => Ps' phosphoramidate having a sequence complementary to part of the telomere-binding region (TBR) of the RNA component of telomerase, so as to inhibit its activity. The N3' => Ps' oligonucleotide phosphoramidates are used therapeutically to inhibit cell proliferation, e.g. against a wide range of solid tumours or leukaemia, and also against fungal and protozoal pathogens. They are soluble and resistant to nuclease, and they bind strongly to RNA forming short but stable duplaxes under physiological conditions. Thus they are sequence represents a specific example of an oligonucleotide N3' => Ps' phosphoramidate disclosed in the specification.
                                                                                            Treating elevated telomerase levels with N3 to P5 oligonucleotide phosphoramidates - that bind to the RNA component of telomerase, specifically for preventing growth of cancer cells, fungi and
                                                                                                                                                                                                                                                                    Claim 5; Page 25; 38pp; English.
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## Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;

ö Gaps ö 100.0%; Score 11; DB 18; Length 11; 100.0%; Pred. No. 2.1e+03; Indels ö 0; Mismatches

DNA oligonucleotide 6, used in the measurement of Tm values.

Peptide nucleic acid; PNA; cancer; telomerase; probe; hybridisation; inhibitor; human telomerase RNA; hTR; PCR; oligonucleotide; ss.

Wright WE Shay JW, Piatyszek MA,

New peptide nucleic acids hybridising to mammalian telomerase used to inhibit telomerase, for treating tumours and other proliferative diseases, also for diagnosis

This sequence is a novel peptide nucleic acid (PNA), which acts as an inhibitor of mammalian, preferably human, telomerase. The PNAs hybridise specifically to an RNA component of mammalian telomerase, and include the sequence GGG for specific hybridisation to the template region of this component. PNAs can be used as probes to detect the RNA component of mammalian telomerase and as inhibitors of telomerase activity, especially in the treatment of cancer.

Seguence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;

New peptide nucleic acids hybridising to mammalian telomerase RNA used to inhibit telomerase, for treating tumours and other proliferative diseases, also for diagnosis

Claim 9; Page 59; 76pp; English.

Wright WE;

Shay JW,

Piatyszek MA,

Norton JC,

Corey D,

(GERO-) GERON CORP.

WPI; 1997-512647/47

96US-0630019 97WO-US05931

39-APR-1996; 09-APR-1997;

Example 2; Page 49; 76pp; English.

This is an oligonucleotide used in the measurement of Tm values and their complimentary peptide nucleic acids (PNAs), (e.g. AAT89231-T89240). FNAs hybridise specifically to an RNA component of

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used
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"Sugar-phosphate backbone has been replaced by
a peptide backbone"
hybridisation to the template region of this component. PNAs can be as probes to detect the RNA component of mammalian telomerase and as inhibitors of telomerase activity, especially in the treatment of
                                                                                     Gaps
                                                                                                                                                                                                                                              Peptide nucleic acid; PNA; cancer; telomerase; probe; hybridisation; inhibitor; ss.
                                                                                                                                                                                                                                                                                                                                                                                     /*tag= c
/note= "Optionally conjugated to peptide AAW31919"
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/note= "Optionally conjugated to peptide AAW31919"
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0
                                                                  Length 11;
                                                                                                                                                                                                                                Peptide nucleic acid 12, targeted to mammalian telomerase.
                                                                                     0; Indels
                                                                  100.0%; Score 11; DB 18; 100.0%; Pred. No. 2.1e+03;
                                               Sequence 11 BP; 4 A; 5 C; 0 G; 2 T; 0 other;
                                                                                    0; Mismatches
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                                                                                                                                                                         AAT89237 standard; DNA; 11
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                                                                                                        1 GTTAGGGTTAG 11
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AAA37556 standard; DNA; 11

4AA37556

15-AUG-2000

AAA37556;

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                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            comprises amplifying a sample with a telomerase primer, e.g. the present sequence, and contacting the product with 1st and 2nd oligonucleotides, which hybridise to the product so that no single stranded region intervenes between them. The hybridised product and oligonucleotides are then contacted with ligase and the ligated form of the oligonucleotides detected.

The method can be used to detect cancer, e.g. carcinomas of the breast, colon, oesophagus, kidney, liver, lung, ovaries, prostate, stomach, uterus, pancreas and head and neck, sarcomas of bone and muscle, leukaemias, myelomas, lymphomas, neuroblastomas, astrocytomas, gliomas, glioblastomas, neuroblastomas and melanomas. The method can also be used to screen for
                                                                                                                                                                                                                                                                                                  Detection; telomerase; amplification; polymerase chain reaction; PCR; primer; cancer; carcinoma; sarcoma; leukaemia; leukemia; meuroblastoma; astrocytoma; glioma; glioblastoma; retinoblastoma; melanoma; screen; drug; determination; telomere length; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting telomerase activity by ligation sequential reaction - useful for diagnosis of cancer or to screen for telomerase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A novel method of detecting telomerase activity in a sample,
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   Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 11; DB 18; Length 11; 100.0%; Pred. No. 2:1e+03; ive 0; Mismatches 0; Indels
                                  Indels
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   100.0%; Score 11; DB 18; 100.0%; Pred. No. 2.1e+03;
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                                Mismatches
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                                                                                                                                                                         AAT90060 standard; DNA; 11 BP
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                                11; Conservative
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                      Telomerase primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inhibitors
                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                        AAT90060;
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cancers, neoplasia, hyperplasia, neurodegenerative diseases, aging, human imay be used the uncodegenerative diseases, aging, human immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency syndroms) and associated pathologies, fungal infections, and other consistency diseases characterized by abnormal telomere metabolism or telomerase activity, in combination with antineoplastic and other cytotoxic or cytostatic agents, antifungal agents, and other nucleotides. PNNs may be used for molecular diagnostics, labelled PNNs are used as hybridization probes to detect or quantitate polyucolectides having a human telomerase of individuals, e.g. paternity testing, based on hTR gene restriction fragment length polymorphism (RRLP) pattern. PNNs are also useful as probes to detect the RNA component of a mammalian telomerase and as probes to detect the RNA component of a mammalian telomerase and as inhibitors of telomerase activity. The method of the present invention allows cancerous conditions to be detected with increased confidence and possibly at an earlier stage, before cells are detected as cancerous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a peptide nucleic acid molecule which phybridises to the mRNA component of mammalian telomerase, and inhibits telomerase activity. Telomerase is a ribonucleoprotein enzyme that synthesizes one strand of the telomeric DNA, using as a template an inucleotide sequence contained within the RNA component of the enzyme. The invention relates to PNA molecules having a sequence of no more than 25 bases, which include the sequence GTTAGG. The uncharged nature of the PNA increases the melting temperature of associating strands, increases the resistence of degradation by proteases or nucleases. The therapeutic PNAs may be used for treating disease conditions such as
                                                                                                                                                                                                                                                                                                                                                                       "Peptide nucleic acid molecule, where N-(2-aminoethyl)glycine units are linked to nucleotide bases via glycine amino N through a methylenecarbonyl linker"
                                                                                                                                               Peptide nucleic acid, PNA; telomerase; ribonucleoprotein enzyme; canci
inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;
AIDS; HIV; fungal infection; forensic identification; detect; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New peptide nucleic acid (PNA) compounds that inhibit telomerase activity in mammalian cells is useful as probes to detect the RNA component of a mammalian telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Piatyszek MA, Shay JW, Norton JC, Corey DR;
                                                                                                      PNA sequence #13 used to inhibit telomerase activity.
                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; Column 71; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96US-0630019.
                                                             (first entry)
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                                                                                                                                                                                                                     paternity testing; ss.
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                                                                                                                                                                                                                                                                                                       Key
misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-APR-1997;
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Gaps

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11; Conservative

Matches

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GTTAGGGTTAG 11

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Gaps

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Indels

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Mismatches

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Query Match
Best Local Similarity
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Local Similarity

8 8

Length 11;

100.0%; Score 11; DB 21; 100.0%; Pred. No. 2.1e+03;

Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;

based on pathological characteristics. The diagnostic and prognostic methods of the present invention can be used to detect an immortal or neoplastic cell or tumour tissue or cancer of any origin, provided the cell expresses telomerase activity and its RNA component.

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The present sequence represents a peptide nucleic acid molecule which hybridises to the mRNA component of mammalian telomerase, and inhibits telomerase activity. Telomerase is a ribonucleoprotein enzyme that synthesizes one strand of the telomeric DNA, using as a template an 11 nucleotide sequence contained within the RNA component of the enzyme. The hivertion relates to PNA molecules having a sequence of no more than 25 bases, which include the sequence GTMAGG. The uncharged nature of the PNA backbone increases the melting temperature of associating strands,
                                                                                                                                                                                                                                                                                                                                                     Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer;
inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;
AIDS; HIV; fungal infection; forensic identification; detect; tumour;
paternity testing; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'G residue is linked to the carboxy end of the peptide GGRQIKIWFQNNMKWKK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-(2-aminoethyl) glycine units are linked to
nucleotide bases via glycine amino N through
methylenecarbonyl linker"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
"Peptide nucleic acid molecule, where
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                                                                                                                                                                                                                                                                                      PNA sequence #18 used to inhibit telomerase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shay JW, Norton JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9; Column 71-72; 45pp; English.
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                                                                                   AAA37561 standard; DNA; 11 BP.
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                                                                                                                                                                                                                 15-AUG-2000 (first entry)
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increases the rate of degradation by proteases or nucleases. The characterized resistance of degradation by proteases or nucleases. The characterized neoplasia, hyperplasia, neurodegenerative diseases, aging, human immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency syndrome) and associated pathologies, fungal infections, and other syndrome) and associated by abnormal telomere metabolism or telomerase activity, in combination with antinoplastic and other cytotoxic or cytostatic agents, antifungal agents, and other nucleotides. PhAs may be used for molecular disapostics, labelled PNAs are used as hybridization probes to detect or quantitate polynucleotides having a human telomerase NA, (HTR) sequence. PNA probes are also used for forensic identification fragment length polymorphism (FFLP) pattern. PNAs are also useful as probes to detect the RNA component of a mammalian telomerase and as inhibitors of telomerase activity. The method of the present invention allows cancerous conditions to be detected with increased confidence and possibly at an earlier stage, before cells are detected as cancerous conditions to be detected with increased confidence and possibly at an earlier stage, before cells are detected as cancerous conditions to be detected with increased confidence and possibly at an earlier stage, before cells are detected as cancerous conditions to be used to detect an immortal or neoplastic cell or tumour tissue or cancer of any origin, provided the cell expresses telomerase activity and its RNA component.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer; inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia; AIDS; HIV; fungal infection; forensic identification; detect; tumour; paternity testing; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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"G residue is linked to the amino end of
peptide GGRQIKIWFQNNMKWKK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 11; DB 21;
100.0%; Pred. No. 2.1e+03;
cive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA37562 standard; DNA; 11 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96US-0630019
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/*tag=
/note= '
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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Best Local S
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Wright WE, Piatyszek MA, Sh

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New peptide nucleic acid (PNA)

Cativity in mammalian cells is

Cativity in mammalian cells

Cativity in compone

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invention relates to PNA molec

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Corey DR; Shay JW, Norton JC,

New peptide nucleic acid (PNA) compounds that inhibit telomerase activity in mammalian cells is useful as probes to detect the RNA component of a mammalian telomerase

Claim 9; Column 71-72; 45pp; English.

The present sequence represents a peptide nucleic acid molecule which hybridises to the mRNA component of mammalian telomerase, and inhibits telomerase activity. Telomerase is a ribonucleoprotein enzyme that synthesizes one strand of the telomeric DNA, using as a template an 11 nucleotide sequence contained within the RNA component of the enzyme. The invention relates to PNA molecules having a sequence of no more than 25 accepts. The mucleotide sequence contained within the RNA component of the enzyme. The invention relates to PNA made and association with targeted nucleic acids, and a fafords greater resistance of association with targeted nucleic acids, and a fafords greater resistance of degradation by proteases or nucleases. The increases the melting temperature of association with targeted nucleic acids, and a fafords greater resistance of degradation by proteases or nucleases. The increases the rate of association with targeted nucleic acids, and a fafords greater resistance of degradation by proteases or nucleases. The cancers, neoplasia, hyperplasia, neurodegenerative dimmunodeficiency virus (HIV) infection/ALDS (acquired immunodeficiency syndrome) and associated pathologies, fungal infections, and other cyclocoxic or diseases characterized by abnormal telomer metabolism or telomerase activity, in combination with antinooplastic and other cyclocoxic or cycostatic agents, antifungal agents, and other nucleotides. PNAs may be used for molecular diagnostics, labelled PNAs are used as hybridization probes to detect tor quantitate polynucleotides having a human telomerase of telomerase activity. The method of the present invention of probes to detect the RNA component of a mammalian telomerase and as inhibitors of telomerase activity. The method of the present invention and propositic and prognostic methods of the present invention can be used to detected as cancerous conditions to be detected with increased confidence of methods of the present invention can be used to detect an immore of cell expresses telo

Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;

Gaps ö 100.0%; Score 11; DB 21; Length 11; 100.0%; Pred. No. 2.1e+03; ive 0; Mismatches 0; Indels

ö

PNA sequence #31 used to inhibit telomerase activity.

Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer; inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia; AIDS; HIV; fungal infection; forensic identification; detect; tumour; paternity testing; ss.

/note= "Peptide nucleic acid molecule, where

Location/Qualifiers

nucleotide bases via glycine amino N through a methylenecarbonyl linker" N-(2-aminoethyl)glycine units are linked

US6046307-A

04-APR-2000

09-APR-1997;

97US-0838545.

96US-0630019. 09-APR-1996;

(TEXA ) UNIV TEXAS SYSTEM.

Corey DR;

Wright WE, Piatyszek MA, Shay JW, Norton JC,

WPI; 2000-292432/25.

New peptide nucleic acid (PNA) compounds that inhibit telomerase activity in mammalian cells is useful as probes to detect the RNA component of a mammalian telomerase

Example 2; Column 33; 45pp; English.

C thoracase activity. Telomerase is a ribonucleoprotein enzyme that telomerase activity. Telomerase is a ribonucleoprotein enzyme that telomerase activity. Telomerase is a ribonucleoprotein enzyme that synthesizes one strand of the telomeric DNA, using as a template an 11 nucleotide sequence contained within the RNA component of the enzyme. The invention relates to RNA melecules having a sequence of no more than 25 bases, which include the sequence drawing a sequence of no more than 25 concers which include the sequence drawing a sequence of no more than 25 bases, which include the sequence drawing a sequence of the PNA backbone increases the melting temperature of associating strands, increases the rate of association with targeted nucleic acids, and affords greater resistance of degradation by proteases or nucleases. The cancers, neoplasia, hyperplasia, neurodegenerative diseases. The cancers, neoplasia, hyperplasia, neurodegenerative diseases. The cancers is neoplasia, hyperplasia, neurodegenerative diseases. Aging, human immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency virus (HIV) infection/AIDS are used for molecular diagnostic and other nucleotides with incincerase activity testing, based on hTR sequence. PNA probes are also used for forensic invention can be fore cells are detected as cancerous conditions to be detected with increased confidence and allows cancerous conditions to be detected with increased confidence and allows cancerous conditions to b The present sequence represents a peptide nucleic acid molecule which hybridises to the mRNA component of mammalian telomerase, and inhibits

Sequence 11 BP; 4 A; 5 C; 0 G; 2 T; 0 other;

ö 100.0%; Score 11; DB 21; Length 11; 100.0%; Pred. No. 2.1e+03; Indels 0; Mismatches 11; Conservative Best Local Similarity Query Match Matches

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Gaps

1 GTTAGGGTTAG 11 

à

AAA37586 standard; DNA; 11 AAA37586 ID AAA3 XX AC AAA3 XX DT 15-2 RESULT 9

BP.

AAA37586;

15-AUG-2000 (first entry)

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Antisense sequence #44 used to inhibit telomerase activity.
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Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer; infinibitor; neoplasia; neurodegenerative disease; aging; hyperplasia; AIDS; HIV; fungal infection; forensic identification; detect; tumour; paternity testing; ss.

Synthetic

Location/Qualifiers ...11 /\*tag= misc\_feature

/\*tag= a /note= "Phosphorothioate internucleotide linkages"

US6046307-A

04-APR-2000

97US-0838545. 09-APR-1997; 96US-0630019 09-APR-1996;

(TEXA ) UNIV TEXAS SYSTEM

Shay JW, Norton JC, Piatyszek MA, Wright WE,

WPI; 2000-292432/25.

New peptide nucleic acid (PNA) compounds that inhibit telomerase activity in mammalian cells is useful as probes to detect the RNA component of a mammalian telomerase -

Example 1; Column 27-28; 45pp; English.

The present sequence represents an antisense oligonucleotide used as a control sequence alongside a peptide nucleic acid molecule which hybridises to the mRNA component of mammalian telomerase, and inhibits telomerase activity. Telomerase is a ribonucleoprotein enzyme that telomerase activity. Telomerase is a ribonucleoprotein enzyme that strands of the telomeric DNA, using as a template an 11 nucleotide sequence contained within the RNA component of the enzyme. The invention relates to PNA molecules having a sequence of no more than 25 bases, which include the sequence GTTAGG. The unchanged nature of the PNA backbone increases the melting temperature of associating strands, increases the rate of association with targeted nucleic acids, and afformed presert resistance of degradation by proteases or nucleases. The therapeutic PNAs may be used for treating disease conditions such as afformed inmunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency syndrome) and associated pathologies, fungal infections, and other immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency syndrome) and associated pathologies, fungal infections, and other cytocoxic or cyctostatic agents, antifungal agents, and other nucleotides. PNAs may be detect or molecular diagnostics, labelled PNAs are used as hybridization or probes to detect or quantitete polymuleotides having a human telomerase activity, in combination with increased on hTR gene restriction of fragment length polymorphism (RPLD) pattern. PNAs are also used as probes to detect the RNA component of a mammalian telomerase and as probes to detect the RNA component of a mammalian telomerase and as probes to detect the RNA component of a mammalian telomerase and as inhubitors of telomerase activity. The method of the present invention can be used to detect an immortal or necessary continued to based on pathological characteristics. The diagnostic an immortal or neoplastic cell expresses telomerase activity and its RNA component.

Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;

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                                        Gaps
                                      ö
100.0%; Score 11; DB 21; Length 11; 100.0%; Pred. No. 2.1e+03; Azive 0; Mismatches 0; Indels
 Query Match
Best Local Similarity 100.(
Matches 11; Conservative
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AAH26728 standard; DNA; 11 BP.

RESULT 11 AAH26728 ID AAH26

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The present sequence was synthesised in an example illustrating an invention relating to polynucleotides comprising a non-homopolymeric sequence of nucleoside subunits joined by at least one inter-subunit linkage that is a N<sup>2</sup>-F<sup>2</sup> thiophosphoramidate. The thiophosphoramidate oligonucleotides retain a high RNA binding affinity and exhibit a much higher acid stability. They are useful for detecting a specific sequence in a sample, by forming a hybridisation complex with the sequence. They are useful for inhibiting function of an RNA in a call (for inhibiting translation of a medicament for translation of a maxNA or for inhibiting telomerase enzyme in a call). They are also useful in the preparation of a medicament for treatment of viral infection or cancer. The oligonucleotides are useful for anti-sense and anti-gene diagnostic or therapeutic applications and may be used for treating telomerase-mediated conditions or diseases, such as
                                                                                                                                                                                                                                                                        Thiophosphoramidate oligonucleotide, virucide, cytostatic, immunosuppressive, contraceptive, RNA inhibitor, telomerase inhibitor, antisense therapy, viral infection, cancer, hyperproliferative disorder, autoimmune disorder, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel thiophosphoramidate polynucleotide useful for detection of RNA or DNA having a given target sequence, for inhibiting RNA function in a cell, and for treating cancer and viral infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rreating telomerase-mediated conditions or diseases, such as hyperproliferative and autoimmune disorders, and for contraceptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                           Oligonucleotide thiophosphoramidate, SEQ ID NO: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;
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                                                                                                                              BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38-SEP-2000; 2000WO-US24688.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0153201.
                                                                                                                              AAF81185 standard; DNA; 11
                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gryaznov S, Pongracz K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Conservative
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GTTAGGGTTAG 11
                                   1 GTTAGGGTTAG 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-265967/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GERO-) GERON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                               WO200118015-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-SEP-1999;
19-OCT-1999;
                                                                                                                                                                                                      30-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                   AAF81185;
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                                                                                             RESULT 10
                                                                                                                AAF81185
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AAH26732 standard; DNA; 11 BP.

2'-arabino-fluorooligonucleotide; phosphoramidate; telomerase; inhibitor; infection; cancer; diagnosis; therapy; cytostatic; virucide; antisense; antigene; ss.

/note= "2'-arabino-fluoronucleosides"

Location/Qualifiers /\*tag= a /mod\_base= "OTHER"

Key modified\_base

Synthetic.

Phosphoramidate-linked 2'-arabino-fluorooligonucleotide.

26-NOV-2001 (first entry)

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Polynucleotides, used to detect and isolate nucleic acids, inhibit function of RNA and telomerase enzymes and to treat e.g. viral infections, contain 2'-arabino-fluoronucleoside(s) linked to
                                                                                                                           'note= "phosphoramidate linkage"
                                                                                                                     /mod_base= "OTHER"
                                                                                                                                                              19-JAN-2001; 2001WO-US01918.
                                                                                                                                                                          21-JAN-2000; 2000US-178248P.
                                                                                                          2..11
/*tag= b
                                                                                                                                                                                                  Gryaznov S, Schultz RG;
                                                                                                                                                                                                                                                                                                                                                                                                               GTTAGGGTTAG 11
                                                                                                                                                                                                             WPI; 2001-589652/66.
                                                                                                                                                                                      (GERO-) GERON CORP.
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                       WO200153307-A1
                                                                                                                                                                                                                                           nucleoside(s)
                                                                                                         modified_base
                                                                                                                                                   26-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                        Matches
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The present sequence is that of a N3'-P5' 2'-arabino-fluoro phosphoramidate oligomuclectide that is complementary to telomerase RNA. The oligomuclectide was used to assess the relative efficacy of novel 2'-arabino-fluoro phosphoramidate oligomuclectides and their 2'-ribo fluorooligomuclectide counterparts (see AAH2728-35) for the inhibition of telomerase cutivity. Novel phosphoramidate 2'-arabino-fluorooligomuclectides are generally more acid stable, more resistant to cellular proteases, and also show greater telomerase inhibition activity than 2'-ribose-fluoro phosphoramidates. They are therefore useful contracting cancer (claimed) and other diseases in which telomerase activity is present at abnormal levels, such as hyperpoliferative or autoimmune diseases e.g. psoriasis, rheumatoid arthritis. Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other; treatment of viral infection (claimed). Example 6; Page 46; 61pp; English.

ö Сарв Length 11; 100.0%; Score 11; DB 22; 100.0%; Pred. No. 2.1e+03;

ö 0; Indels 0; Mismatches 11; Conservative GTTAGGGTTAG 11

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The present sequence is that of a 2'-ribose-fluoro
phosphoramidate oligonucleotide that is complementary to
telomerase RNA. The oligonucleotide was used to assess the
relative efficacy of novel 2'-rarbino-fluoro phosphoramidate
relative efficacy of novel 2'-ribose fluorophosphoramidate
counterparts (see AAH2728-35) for the inhibition of telomerase
conterparts (see AAH2728-35) for the inhibition of telomerase
activity. Novel phosphoramidate 2'-rarbino-fluorophosphoramidate
counterparts (see AAH2728-35) for the inhibition of telomerase
cotivity. Novel phosphoramidate 2'-rarbino-fluorophosphoramidates
cotivity and also show greater telomerase inhibition activity
than 2'-ribose-fluoro phosphoramidates. They are therefore useful
contracting cancer (claimed) and other diseases in which telomerase
activity is present at abnormal levels, such as hyperproliferative
or autoimmune diseases e.g. psoriasis, rheumatoid arthritis,
immune system disorders requiring immunosuppression, and in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polynucleotides, used to detect and isolate nucleic acids, inhibit function of RNA and telomerase enzymes and to treat e.g. viral infections, contain 2'-arabino-fluoronucleoside(8) linked to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                 2'-ribose-fluorooligonucleotide; phosphoramidate; telomerase;
inhibitor; infection; cancer; diagnosis; therapy; cytostatic;
virucide; antisense; antigene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 11;
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                                                                                                 Phosphoramidate-linked 2'-ribose-fluorooligonucleotide.
                                                                                                                                                                                                                                                                                                         'note = "2'-ribose-fluoronucleosides"
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                                                                                                                                                                                                                                                                                                                                                         /mod_base= "OTHER"
/note= "phosphoramidate linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;
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                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                       2..11
/*tag= a
/mod_base= "OTHER"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 6; Page 46; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JAN-2001; 2001WO-US01918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JAN-2000; 2000US-178248P
                                                                                                                                                                                                                                                                                                                           2..11
/*tag= b
                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gryaznov S, Schultz RG;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleoside(s) -
                                                                                                                                                                                                                                                                                                                                                                                                            WO200153307-A1
                                                                                                                                                                                                                                                      modified base
                                                                                                                                                                                                                                                                                                                           modified base
                                                                 26-NOV-2001
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                                                                                                                                                                                                      Synthetic
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RESULT 13

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Gaps

RESULT 12 AAH26732

Gaps

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Length 11; 0; Indels

AAS14909

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Claim 1; Page 37; 74pp; English.
                                                                                                30-MAR-2001; 2001WO-US10162.
                                                                                                      31-MAR-2000; 2000US-0540843
            14-FEB-2002 (first entry)
                                                                                                                                                                                                                            method of the invention
                                                                                                                         WPI; 2001-626338/72.
                                                                                                            (UYBO-) UNIV BOSTON.
                                                                                   WO200174342-A2
                                                       modified_base
                                                                    modified base
                                                                                                                  Gilchrest BA,
                                                                                         11-OCT-2001
                                              Synthetic.
     AAS14909;
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proliferation by treating cells with at least one oligonucleotide, or its fragment. The compounds, which have cytostatic, anti-allergic, anti-inflammatory, dermatological, auti-postratic and immunosuppressive activities, function as 'ultra-violet mimics' to induce DNA repair processes (or a protective response to later exposure to DNA repair processes (or a protective response to later exposure to Tradiation or chemicals), as a proliferation inhibitor, apoptosis inducer or a tumour necrosis factor inhibitor. Probably they mimic products of DNA damage, or processed DNA-damage intermediates, by inducing the p53 pathway, resulting in transient arrest of cell growth, allowing more time for DNA repair to occur before cell division takes place. The method is especially used to treat carcinoma but may also be used to: treat other C hyperproliferative states (e.g. psoriasis or precancerous conditions); reduce photoaging, oxidative stress or damage; prevent skin cancer; treat allergically mediated inflammation (atopic or contact dermatitis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              anti-inflammatory; dermatological; ophthalmological; anti-psoriatic; immunosuppressive; DNA repair; proliferation inhibitor; apoptosis; immunosuppressive; DNA repair; proliferation inhibitor; apoptosis; carcinome, oxidative stress; skin cancer; allergy mediated inflammation; conjunctivitis; allergic rhinitis; vitiligo; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inhibiting proliferation of epithelial cells, useful e.g. for treating carcinoma, using specific oligonucleotides that mimic the effects of ultra-violet light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Melanin, melanogenic; oligomer; cytostatic; anti-allergic; p53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention describes inhibition of mammalian epithelial cell
                                                                                  100.0%; Score 11; DB 23; 100.0%; Pred. No. 2.1e+03;
                              Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Melanogenesis associated oligonucleotide #9.
                                                                                                                                               0; Mismatches
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/note= "Phosphorylated"
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AAS14913 standard; DNA; 11 BP.
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                                                                               Query Match
Best Local Similarity
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modified_base
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XS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention describes inhibition of mammalian epithelial cell
proliferation by treating cells with at least one oligonucleotide, or
the first fragment. The compounds, which have cytostatic, anti-allergic,
anti-inflammatory, dermatological, ophthalmological, anti-allergic,
anti-inflammatory, dermatological, ophthalmological, anti-allergic,
immunosuppressive activities, function as 'ultra-violet mimics' to induce
the parair processes (or a protective response to later exposure to
radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
or a tumour necrosis factor inhibitor. Probably they mimic products of
the parair to occur before cell division takes place. The method is
pathway, resulting in transient arrest of cell growth, allowing more time
for DNA repair to occur before cell division takes place. The method is
compared to treat carcinoma but may also be used to:
thyperproliferative states (e.g. psoriasis or precancerous conditions);
reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
allergically mediated inflammation (atopic or contact dermatitis,
cells caused by radiation or chemicals; increase melanin production
colls on promote apoptosis in epithelial cells (e.g. for treating vitiligo), and to
promote apoptosis in response to DNA damage, in epithelial cells that
contain damaged by radiation or chamicals;
sequence is melanogenessis and conjugnocleotide #5, representative
confinitis menanogenessis and coligonucleotide #5, representative
confinitis melanogenessis and one of the oligonucleotides used
conjuder to inhibit mammanian epithelial cell proliferation, described in the
                                                                                                                                                                                                                                                             Melanin, melanogenic; oligomer; cytostatic; anti-allergic; p53; anti-inflammatory; dermatological; ophthalmological; anti-psoriatic; immunosuppressive; DNA repair; proliferation inhibitor; apoptosis; tumour necrosis factor inhibitor; photoaging; hyperproliferative disease; carcinoma; oxidative stress; skin cancer; allergy mediated inflammation; conjunctivitis; allergic rhinitis; vitiligo; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inhibiting proliferation of epithelial cells, useful e.g. for treating carcinoma, using specific oligonucleotides that mimic the effects of ultra-violet light -
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/note= "Optionally phosphorylated"
                                                                                                                                                                                                      Melanogenesis associated oligonucleotide #5.
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/*tag= b
/mod_base= OTHER
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                           AAS14909 standard; DNA; 11 BP
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us-09-540-843-5.szlm30.rng

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AAS15434 standard; DNA; 11 BP.
Obe
Obe
Okasistaa
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(pigmentation) in epithelial cells (e.g. for treating vitiligo), and to promote apoptosis in epithelial cells that contain damaged DNA. Also oligonuclectides that contain non-hydrolyzable backbones are used to inhibit apoptosis, in response to DNA damage, in epithelial cell. This sequence is melanogenesis associated oligonuclectide #9, one of the oligonuclectides used to inhibit mammalian epithelial cell proliferation, described in the method of the invention.
cells caused by radiation or chemicals; increase melanin production
888888888888
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Sequence 11 BP; 4 A; 5 C; 0 G; 2 T; 0 other;

ö Gaps ö Length 11; 0; Indels 100.0%; Score 11; DB 23; 100.0%; Pred. No. 2.1e+03; 0; Mismatches 1 Similarity 100. Query Match Best Local S Matches

1 GTTAGGGTTAG 11 GTTAGGGTTAG 1

AAS15434;

(first entry) 14-FEB-2002

PNA 7/IV inhibiting human and mammalian telomerase activity.

Mammalian; peptide nucleic acid; probe; forensic; paternity testing; human telomerase RNA component; hTR gene RFLP pattern; cancer; inflammation; lymphoproliferative disease; autoimnume disease; neurodegenerative disease; neoplasia; hyperplasia; HIV; AIDS; human immunodeficiency virus; acquired immunodeficiency syndrome; telomere metabolism; mutant; cytóstatic; anti-inflammatorý; immunosuppressive; polyamide backbone; ss.

Homo sapiens Synthetic.

Location/Qualifiers Key modified\_base

acid, i.e. it /\*tag= a /note= "This sequence is a peptide nucleic acid, i contains a polyamide backbone instead of a

US6294650-B1

25-SEP-2001.

99US-0349532. 38-JUL-1999;

97US-0838545. 96US-0630019. 09-APR-1996; 39-APR-1997;

(TEXA ) UNIV TEXAS SYSTEM.

Norton JC Corey DR, Piatyszek MA, Shay JW, Wright WE,

WPI; 2001-638024/73

New peptide nucleic acids that hybridizes to the RNA component of mammalian telomerase, useful for treating or preventing cancer, inflammation, lymphoproliferative diseases, autoimmune disease, or neurodegenerative diseases

Claim 7; Column 73; 46pp; English.

The present invention relates to peptide nucleic acids (PNAs), comprising a sequence of 6-25 nucleobases, that inhibit telomerase activity in mammalian cells by hybridising to the RNA component of mammalian

telomerase. The PNAs are useful as probes to detect the RNA component of mammalian telomerase and as inhibitors of telomerase activity, or to detect and/or quantitate polynucleotide having the human telomerase RNA component (hTR) sequence, as well as in forenaic identification of individuals, such as paternity testing or identification of criminal suspects or unknown descendants based on the hTR gene RFLP pattern. The PNA can be further used for treating or preventing cancer, inflammation, lymphoproliferative diseases, autoimmune disease, or neurodegenerative diseases. The PNAs in combination with other pharmaceuticals (such as antineoplastic or cytostatic agents) can be used for treating neoplasia, hyperplasia, human immunodeficiency virus (HIV) infections, acquired immunodeficiency sylving associated pathologies, and other diseases characterised by abnormal telomere metabolism or telomerase activity. The present sequence represents one of the PNA sequences of the invention. 88888888888888888888888

Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;

Gaps ö Length 11; Indels 100.0%; Score 11; DB 23; 100.0%; Pred. No. 2.1e+03; iive 0; Mismatches 0; Query Match
Best Local Similarity 100.0%;
Matches 11; Conservative

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11 GTTAGGGTTAG 11 1 GTTAGGGTTAG 쉱 à

Search completed: December 31, 2003, 15:08:14 Job time : 317,886 secs

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AZ514597 1M0351E14
B1945 MUSGSS01807
B1945 MUSGSS01807
AZ766315 1M0563X14
AL92458 T. brucei
AV544203 AV544203
AV544203 AV544203
AV544203 AV544203
AL355344 ALU255344
L132043 HUMXP2G6A H
AZ789554 AM0255826
AZ778302 SAMC 7038
BE385567 601275826
AZ778302 SAMC 7038
BE385567 601275826
AZ778302 SAMC 2038006
AZ778302 SAMC 2038006
AZ7785529 SAMC 2038009
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AZ759617 1M0552M20
AZ759617 1M0554P21
AZ810596 1M0508M23
AZ862703 1M0564D21
AZ813982 ZM01186E12
AZ462640 1M0269L11
AZ827252 ZM0103905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AZ614760 19 bp DNA linear GSS 13-DEC-2000 1M0443A17R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0443A17 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)

Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R.,

M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A.,

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished
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University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                        AZ766315
TA319C11P
AU256889
AV544203
TA274G11Q
AU255344
                                                                                                                                              AZ761166
AZ778302
BH000596
AZ770857
AZ623979
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AZ759615
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D18745
BH907981
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AZ789654
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AZ833982
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
 AZ614760
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AZ614760
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DEFINITION
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 AZ614760 1M0443A17
AL472050 T. brucei
AL462065 T. brucei
AZ803795 2M0064D22
                                                                     December 31, 2003, 13:58:09 ; Search time 1263.89 Seconds (without alignments) 211.530 Million cell updates/sec
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                                                                                                                                                                                                               33330
         GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                               Gapop 10.0, vayer, ...

Gapop 10.0, vayer, ...

Gapop 10.0, vayer, ...

Searched: 22781392 seqs, 12152238056 residues

Frotal number of hits satisfying chosen parameters:

Hinimum DB seq length: 0

Aaximum DB seq length: 30

Aaximum Match 0$

Maximum Match 100$

Listing first 45 summaries
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TA158A03P
TA84A06P
AZ803795
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No.
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5

O O

Std Error: 0.00

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0 Plate: 0443 row: A column: 17 Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends ends top: 19. Location/Qualifiers

FEATURES

organism="Mus musculus" /mol\_type="genomic DNA" /strain="C57BL/6J" 'db xref="taxon:10090"

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Query Match
Best Local Similarity
Matches 11; Conserval
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                                                                                                                    Similarity
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TA84A06P
                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
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                                                                                                                                (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch oritice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwaye2 (gql 4772114[gb]AR12972.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli Xiii0-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TA158A03P 20 bp DNA linear GSS 13-DEC-2000 T. brucei sheared genomic DNA clone 158a03, forward sequence,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Rrypanosoma brucei (TREU927)4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                     /clone_lib="Mouse 10kb plasmid UUGCIM library"
//note="Vector: PWD42rv; Purified genomic DNA from M.
musculus C57BL/67 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                  sex="Male"
lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 11; DB 28; Length 19; 100.0%; Pred. No. 1.5e+04; tive 0; Mismatches 0; Indels
clone="UUGC1M0443A17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genomic survey sequence.
AL472050
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Best Local Similarity 100.
Matches 11; Conservative
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בהסיואטטר 25 bp DNA linear GSS 13-DEC-2000
T. brucei sheared genomic DNA clone 84a06, forward sequence,
genomic survey sequence.
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                   insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTAL 10.1) was mechanically sheared
to give a tight size discribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
innsert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
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Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/T_brucei/.
Location/Qualifiers
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Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
described in detail in Smith, H. and Venter, J.C. (Making small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 11; DB 29; 100.0%; Pred. No. 1.5e+04;
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/organism="Trypanosoma brucei"
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                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
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11 c
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VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

RESULT 4 AZ803795/c DEFINITION

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us-09-540-843-5.szlm30.rst

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114[gb]AF129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLLO-Gold (Stratagene) cells and selected for ampicillin resistance."
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84112, USA
                                                                                                                                                                                                                                                    GSS 14-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1 (bases 1 to 22)
                                                                                                                                                                                                                                              AZ666649 10kb plasmid UUGCIM library Mus musculus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Blan, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="Male"
/lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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                                                                                                                                                                                                                                                                                                           clone UUGC1M0548M19 R, genomic survey sequence
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Pred. No. 1.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plate: 0548 row: M column: 19
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends

    .22
    /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 801 585 5606
Fax: 801 585 7177
                                  GTTAGGGTTAG 11
                                                                                            26 GTTAGGGTTAG 16
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Best Local Similarity
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AUTHORS
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Malam, L., Longacret, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, M., Stokes, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                           AZ803795
2M0064D22F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0064D22 F, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 27.
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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University of Utah Genome Center
University of Utah
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Fax: 801 585 7177
GTTAGGGTTAG 11
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USA
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TRANSPORTED TO THE PROPERTY OF THE PROPERTY OF

AZ514597/c DEFINITION

RESULT 6

ACCESSION VERSION KEYWORDS

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D18745 22 bp mRNA linear EST 12-DEC-1995 MUSGS01807 Mouse 3'-directed Mus musculus domesticus cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Kawamoto,S., Okubo,K., Yoshii,J., Katsuki,M. and Matsubara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
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/clone="mittan"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)
Awamoto,S., Okubo,K., Yoshii,J., Katsuki,M. and Matsubara,K. Analysis of gene expression in mouse embryogenesis by 3'-directed Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, F., Zimmeran, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BH907981 SALK 045087.34.20.x Arabidopsis thaliana TDNA insertion lines
SALK 045087.34.20.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_045087.34.20.x, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus domesticus (western European house mouse)
Mus musculus domesticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81.8%; Score 9; DB 14; Length 22;
100.0%; Pred. No. 2.3e+05;
cive 0; Mismatches 0; Indels
                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Institute for Cellular and Molecular Biology

    .22
/organism="Mus musculus domesticus"

     Pred. No. 1.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Osaka University
3-1 Yamada-oka, Suita, Osaka 565, Japan.
Location/Qualifiers
                                 0; Mismatches
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                                                                                                                                                                                                                                                     GSS 05-OCT-2000
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 29)
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Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                          AZ514597
1M0361E14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0361E14 F, genomic survey sequence.
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        Gaps
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        1; Indels
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Fax: 801 585 7177
Email: ddunmogenetics.utah.edu
Insart Length: 10000 Std Error: 0.00
Plate: 0361 row: E column: 14
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Class: plasmid ends
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University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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/clone="UUGC1M0361E14"
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Gaps

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GSS 04-SEP-2002

Shinn, P

Contact: Joseph R. Ecker

COMMENT

85.5%; Score 9.4; DB 28; Length 29;

Query Match

BASE COUNT ORIGIN

us-09-540-843-5.szlm30.rst

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/mol_type="genomic DNA"
                 /db_xref="taxon:10090"
/clone="UUGC1M0563K14"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db kref="taxon:3702"
/clone="SALK 045087.34.20.x"
/clone="Ib="Arabidopsis thaliana TDNA insertion lines"
/clone lib="Arabidopsis thaliana these each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

a 5 c 2 g 6 t
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Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of This is single pass within an annotated intron of At1944820.
Class: TDNA tagged.
Location/Qualifiers
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1M0563K14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0563K14 R, genomic survey sequence.
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/mol_type="genomic DNA"
/strain="Columbia 0"
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Length: 10000 Std Error: 0.00
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/strain="C57BL/63"
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Mus musculus
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalp42 (gil-4732114[gb]AP129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli Xi10-Gold (Stratagene) cells and selected for ampicillin resistance."
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DNA clone 319c11, forward sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTAT 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects.
Barrell, Oxford University Press, 1999).
Bemail: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
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1 (bases 1 to 23)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CBlO 1SA, E-mail: barrell@eanger.ac.uk
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clome_llb="Mouse_lokb plasmid UTGCIM library"
/note="Wector: PWD42Iv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Eukaryota, Buglenozoa, Kinetoplastida, Trypanosomatidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76.4%; Score 8.4; DB 28; 90.0%; Pred. No. 5.2e+05; iive 0; Mismatches 1;
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/organism="Trypanosoma_brucei"
                                                                                                                                                            Laboratory Mouse DNA Resource
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    brucei sheared genomic

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Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREND27/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v+i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayederigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                         Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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                                              A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="roots"
/clone_lib="Arabidopsis thaliana roots Columbia"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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AL485967.1 GI:11851842
GSS.
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1 (bases 1 to 25)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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Pred. No. 5.4e+05;
0; Mismatches 1; Indels
         Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .25
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/strain="Columbia"
/db_xref="texon:3702"
/clone="RZ36a11F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .25
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
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7
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Best Local 8
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TA274G11Q/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
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ORIGIN
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                                                                                                                                                                                                                              MEDLINE
PUBMED
COMMENT
AUTHORS
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KEYWORDS
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1 (bases 1 to 25)
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/tissue type="brain"
/clone_lib="3'-directed mouse cDNA library"
? q 5 t
                                                                                                                                                                                                                                                                                 Length 23;
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Pred. No. 5.4e+05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                             Score 8.4; DB 29; Length 2 Pred. No. 5.3e+05; 0; Mismatches 1; Indels
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Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5589
Email: kkato@bs.aist-nara.ac.jp,
UKL:http://love2.aist-nara.ac.jp,
Location/Qualifiers
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Arabidopsis thaliana
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/organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="BED0009219"
                                              /db_xref="taxon:5691"
/clone="319c11"
                                                                                                                                               3
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (house mouse)
Mus musculus
             strain="TREU927"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AU256889.1 GI:20320970
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AV544203.1 GI:8715617
                                                                                                                                                                                                                                                                        76.4%;
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90.0%;
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Best Local Similarity 90.0
Matches 9; Conservative
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Isolation of chromosome-specific genes by reciprocal probing of arrayed cDNAs and cosmid libraries Hum. Mol. Genet. 4, 1373-1380 (1995) 96090257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone lib="Human placenta"
/note="Arrayed cDNAs and cosmid libraries from human
placental tissue"
                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
/map="Xq21.3; Xq21.3, Yp11.3"
/clone="Xp2G6A"
                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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                                                                                                                                                                                                                                                           Contact: Caskey, C.T.H.
Location/Qualifiers
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            and Caskey, C.T.H.
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Kato, K. and Macoba, R. Generation of expressed sequence tags from mouse brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lee, C.-C., Yazdani, A., Wehnert, M., Bailey, J., Couch, L., Xiong, M., Coolbaugh, M.I., Chinault, C.A., Baldini, A., Lindsay, E.A., Zhao, Z.-Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:10090"
/clone="BED0005210"
/tissue_type="brain"
/clone_lib="3'-directed mouse cDNA library"
3 g 8 t
                                                                                                                                                                                                           76.4%; Score 8.4; DB 29; Length 25; 90.0%; Pred. No. 5.4e+05; tive 0; Mismatches 1; Indels
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Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5581
Fax: 81-743-72-5589
Email: kkato@bs.aist-nara.ac.jp,
URL:http://love2.aist-nara.ac.jp,
Location/Qualifiers
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/db_xref="taxon:5691"
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O Query Match 1 COnservative 90.0%;

Matches 9; Conservative
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Matches 9; Conserv
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Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 11; Conservative 0; Mismatches 0;
                                          US-09-349-532-12
US-08-531-743-4
US-08-630-019A-12
US-08-630-019A-10
US-08-838-545-2
US-08-838-545-5
US-09-349-532-2
US-09-349-532-45
US-09-349-532-45
US-09-349-532-45
US-09-349-532-45
US-08-8119-874-11
US-08-153-051B-11
US-08-119-867-20
US-08-119-867-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MG-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION UNDER: US/08/330,123A
FILING DATE: 27-OCT-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                         US-08-819-867-20
US-08-464-011B-60
US-09-378-535-20
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APPLICATION NUMBER: US 08/272,102
FILLING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,23
REFERENCE/DOCKET NUMBER: 15389-000810
TELECOMMUNICATION IN
                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08330123A
Patent No. 5883016
GENERAL INFORMATION:
APPLICANT: FING, Junil, Bryant
APPLICANT: FING, Junil, APPLICANT: FINK, Walter
APPLICANT: ANDREWS, William H.
TITLE OF INVENTION: HUMAN TELOMERASE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Townsend and To
STREET: 379 Lytton Avenue
CTY: Palo Alto
STATE: California
COUNTRY: US
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TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
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RESULT 1
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                                                                                                                                               December 31, 2003, 14:40:05 ; Search time 42.7468 Seconds (without alignments) 113.581 Million cell updates/sec
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Sequence 36
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Sequence 3
Sequence 3
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Sequence 4
Sequence 2
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(cgn2_6/ptodata/1/ina/5A_COMB.seq:*
(cgn2_6/ptodata/1/ina/5B_COMB.seq:*
(cgn2_6/ptodata/1/ina/6A_COMB.seq:*
(cgn2_6/ptodata/1/ina/6B_COMB.seq:*
(cgn2_6/ptodata/1/ina/RB_COMB.seq:*
(cgn2_6/ptodata/1/ina/RB_COMB.seq:*
(cgn2_6/ptodata/1/ina/RB_COMB.seq:*
                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                           Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Optoral number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Aaximum DB seq length: 30

Optor-processing: Minimum Match 0*
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US-08-462-115B-2
US-08-662-115B-2
US-08-531-743-11
US-08-531-743-12
US-08-531-743-12
US-08-531-743-12
US-08-530-019A-39
US-08-630-019A-39
US-08-938-545-44
US-09-949-532-44
US-09-680-517-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maximum Match 100%
Listing first 45 summaries
                                                                                                         OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Match
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Gaps

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Sequence 11, Application US/08531743
Patent No. 5856096
GENERAL INFORMATION:
APPLICANT: Wind
APPLICANT: Chen, Shi-fong
APPLICANT: Chen, Shi-fong
APPLICANT: Tetcher, Terace M.
APPLICANT: Maine, Ira
TITLE OF INVENTION: Rapid and Sensitive Assays for Detecting and
TITLE OF INVENTION: Distinguishing Between Processive and
TITLE OF INVENTION: No. 5856096-Processive Telomerase Activities
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 11; DB 2; Length 11; 100.0%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                              COUNTRY: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
SOFTWARE: PATENTIN Balease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,678A
FILING APPLICATION: 435
PRIOR APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION NUMBER: US 08/330,123
FILING DATE: US-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000811US
TELECOMMUNICATION INFORMATION:
NAME: STORE OF US O
                                         NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
ADRESSEE: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
        Mammalian Telomerase
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ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Texas
COUNTRY: United States of America
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
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CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GTTAGGGTTAG 11
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    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: RNA
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                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Funk, Walter
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Assays for the RNA Component of Human
TITLE OF INVENTION: Assays for the RNA Component of Human
TITLE OF INVENTION: Assays for the RNA Component of Human
TITLE OF INVENTION: Assays for the RNA Component of Human
TITLE OF INVENTION: Assays for the RNA Component of Human
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TITLE OF INVENTION: Assays for the RNA Component of Human
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100.0%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 11; Conservative 0; Mismatches 0; Indels
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ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,115B
FILING DATE: 07-UW-1995
PRIOR APPLICATION 0435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-UUL-1994
PRIOR APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
APPRICATION NUMBER: 32,944
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR ESQ ID NO:
SEQUENCE CHARACTERISTICS:
TENTING INFORMATION:
TENTING INFORMATION:
TELECOMMUNICATION INF
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; Sequence 2, Application US/08660678A
; Patent No. 5837857N;
; GENERAL INFORMATION;
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Peng, Juni;
; APPLICANT: Peng, Valle
; APPLICANT: Andrews, William H.
                                                                                                                                                                                                         RESULT 2
US-08-482-115B-2/c
; Sequence 2, Application US/08482115B
; Patent No. 5776679
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GTTAGGGTTAG 11
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Gaps

Indels

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                                                                                                                   Length 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Andrews, William H.
APPLICANT: Andrews, William H.
APPLICANT: Arailon, Ariel Athena
APPLICANT: Freng, Junia
APPLICANT: Frong, Junia
APPLICANT: Frong, Junia
APPLICANT: Frong, Maria Antonia Blasco
APPLICANT: Willeponteau, Bryant
TITLE OF INVENTION: RNA COMPONENT OF TELOMERASE
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WEDION TYPE: FIJOPPY disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,778
FILING DATE: 07-JE-1995
RIOR APPLICATION NUMBER: US 08/387,524
FILING DATE: 13-FEB-1995
RIOR APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
RIOR APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
RIOR APPLICATION NUMBER: US 08/310,123
FILING DATE: 07-OCT-1994
RIOR APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
AND ATTORNEY/AGENT ATT
                                                                                                               Score 11; DB 2; I
Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 11; DB 2; I
100.0%; Pred. No. 1.6e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                               0; Mismatches
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REGISTRATION NUMBER: 32,227
REPERENCE/DOCKET NUMBER: CSHL94-05A4
TELECOMMINICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 36, Application US/08485778 Patent No. 5876979
                                                                                                           100.0%;
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INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                   1 GTTAGGGTTAG 11
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US-08-485-778-36/c
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US-08-485-778-36
                                   US-08-531-743-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                   8
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STRANDEDNESS: single

CORPLOGY: linear

Ouery Match

Dest Local Similarity 100.0%; Score 11; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.6+02;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps of 1 GTTAGGGTTAG 11

Dest Local Similarity 100.0%; Pred. No. 1.6+02;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 1 GTTAGGTTAG 11

On 1 GTTAGGGTTAG 11

I GTTAGGGTTAG 11

GENERAL INFORMATION: Bradford E. Septicher, Shi-fong APPLICANT: Windle, Bradford E. APPLICANT: Windle, Bradford E. APPLICANT: Pletcher, Terace M. APPLICANT: Pletcher,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPACTIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PREADIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/531,743
FILING DATE: 20-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: 37,642
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
TELEPAX: (512) 418-3000
TELEPAX: (512) 418-377
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/531,743
FILING DATE: 20-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REGISTRATION NUMBER: 37,642
REPERRONCE/DOCKET NUMBER: CTRC:026/HYL
TELEPHONE: (512) 414-7577
INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
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APPLICANT: Shay, Jerry W.
APPLICANT: Wright, Woodring E.
APPLICANT: Piatyszek, Mieczyslaw A.
APPLICANT: Piatyszek, Mieczyslaw A.
APPLICANT: David
APPLICANT: No. 6015710ton, James C.
TITLE OF INVENTION: Modulation of Mammalian Telomerase by
TITLE OF INVENTION: Peptide Nucleic Acids
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: U$/08/520,550A

FILING DATE: 29-AUG-1995

CLASSIPICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: U$ 08/330,123

FILING DATE: 37-PEB-1995

PRIOR APPLICATION NUMBER: U$ 08/330,123

FILING DATE: 70-C1-1994

PRIOR APPLICATION NUMBER: U$ 08/272,102

FILING DATE: 07-QUL-1994

APPLICATION NUMBER: U$ 08/272,102

FILING DATE: TOWNERT: 32-DS

RESISTATION NUMBER: 32-227

RESISTATION NUMBER: 32-227

RESISTATION NUMBER: SCHL-6240

TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
      Brook, Smith & Reynolds, P.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 11; DB 3; L; Pred. No. 1.6e+02; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9, Application US/08630019A Patent No. 6015710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%;
Matches 11; Conservative 0;
ADDRESSEE: Hamilton, Broo
STREET: Two Militia Drive
CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
US-08-520-550A-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Shay,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94111-3834
                                                                                        STATE: M. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-630-019A-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:

SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/472,802C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION NUMBER: US 08/330,123
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: SMITCH, M1111am M:
REGISTRATION NUMBER: 15389-000820
TELECOMMUNICATION INFORMATION:
                                                                      Sequence 3, Application US/08472802C
; Patent No. 5958680
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
; TITLE OF INVENTION: Mammalian Telomerase
; TITLE OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; CITY: ADITIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDUWTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-520-550A-36/c
; Sequence 36, Application US/08520550A
; Patent No. 6013468
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Marhuenda, Maria A. B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Andrews, William H.
Avilion, Ariel A.
Feng, Junli
Funk, Walter
Greider, Carol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS LENGTH: 11 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GTTAGGGTTAG 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FOR MEDIUM TYPE: Flop COMPUTER READABLE FOR COMPUTER PROFICATION NUMBER FILING DATE: 07-0 FRIOR APPLICATION NUMBER FILING DATE: 07-0 FRIOR APPLICATION DA APPLICATION NUMBER FILING DATE: 27-0 ATPORNEY/AGENT INFOR NAME: SMILTH, WILL REFERENCE/DOCKET NIMBER FOR SECULOR OF APPLICATION NUMBER FOR SECULOR F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Avilion,
APPLICANT: Feng, Ju
APPLICANT: Peng, Ju
APPLICANT: Greider,
APPLICANT: Marhuenc
APPLICANT: Villepor
IITLE OF INVENTION:
                              RESULT 7
US-08-472-802C-3/c
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Gaps

us-09-540-843-5.szlm30.rni

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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 39, Application US/08630019A

Patent No. 6015710

GENERAL INFORMATION:
APPLICANT: Shay, Jerry W.
APPLICANT: Wright, Woodring E.
APPLICANT: Corey, David
APPLICANT: No. 6015710ton, James C.
TITLE OF INVENTION: Modulation of Mammalian Telomerase by
TITLE OF INVENTION: Peptide Nucleic Acids
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "phosphorothioate (PS) nucleic acid"
                                                                                                                                                  Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 11; DB 3; Length 11; 100.0%; Pred. No. 1.6e+02;
                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,019A
FILING DATE: 09-JUN-1996
CLASSIFICATION: 536
                                                                                                                                                  100.0%; Score 11; DB 3; I 100.0%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       015389-001600US
                                                                                                                                                                                                           0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
US-08-838-545-13
'; Sequence 13, Application US/08838545
'; Patent No. 6046307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 0153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ. ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
                                                                                                                                                                                                           11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Conservative
              single
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                    1 GTTAGGGTTAG 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GTTAGGGTTAG 11
                                                                                                                                                                                                                                                                                                                       11 Gringedring 1
                                ; TOPOLOGY: linear;
MOLECULE TYPE: RNA
US-08-630-019A-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 11; Conserva
                                                                                                                                                     Query Match
Best Local Similarity
        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-630-019A-39
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                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               other nucleic acid (PNA), desc = "peptide nucleic acid (PNA), where (deoxy)ribose-phosphate linkages are replaced by N-(2-aminoethy)jycine units linked to nucleotide bases via glycine amino nitrogen through a methylenecarbonyl linker"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Shay, Jerry W.
APPLICANT: Wright, Woodring E.
APPLICANT: Piatyszek, Mieczyslaw A.
APPLICANT: Or 6015710ton, James C.
APPLICANT: No. 6015710ton, James C.
TITLE OF INVENTION: Modulation of Mammalian Telomerase by TITLE OF INVENTION: Peptide Nucleic Acids
NUMBER OF SEQUENCES: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 11; DB 3; Length 11; 100.0%; Pred. No. 1.6e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,019A
FILING DATE: 09-UIN-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Stocella, 32,944
RECISTRATION NUMBER: 32,944
RECISTRATION NUMBER: 32,944
RECISTRATION NUMBER: 32,944
TELECOMMUNICATION INFORMATION:
TELECHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 Dase pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                           015389-001600US
                 UMBER: US/08/630,019A
09-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 30, Application US/08630019A Patent No. 6015710
                                                  FILING DATE: 09-070-37 (2012)
FILING DATE: 09-070-37 (2012)
ATTORNEY/AGENT INFORMATION: NAME: SCOTELLA, JOHN R. REGISTRATION NUMBER: 32,944
REFRENCE/DOCKET NUMBER: 0153F
TELECOMMUNICATION INFORMATION: TELEFAM: (415) 576-0200
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: LENGTH: 11 base pairs TYPE: nucleic acid STRANDENESS: single
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 11; Conservative
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                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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DESCRIPTION:
DESCRIPTION:
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/desc = "peptide nucleic acid (PNA),
where (deoxy(ribose-phosphate linkages are replaced by
N-(2-aminoethyl)glycine units linked to nucleotide bases via
glycine amino N through a methylenecarbonyl linker"
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Sequence 44, Application US/08838545

Patent No. 6046307

GENERAL INFORMATION:
APPLICANT: Wright, Woodring E.
APPLICANT: Wright, Woodring E.
APPLICANT: Corey, David E.
APPLICANT: No. 6046307con, James C.
TITLE OF INVENTION: Modulation of Mammalian Telomerase by TITLE OF INVENTION: Peptide Nucleic Acids
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 11; DB 3; Length 11; 100.0%; Pred. No. 1.6e+02; Live 0; Mismatches 0; Indele
                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/838,545

FILING DATE: 09-APR-1997

CLASSIFICATION NUMBER: US/08/630,019

FILING DATE: 09-APR-1996

ATTONEY APPLICATION NUMBER: US/08/630,019

FILING DATE: 09-APR-1996

ATTONEY APPLICATION NUMBER: 32,944

REGISTRATION STOCKET NUMBER: 015389-001610US

TELEPHONE: (415) 576-0200

INFORMATION FOR SEQ ID NO: 31: SEQUENCE CHARACTERISTICS:

LEMOTH: 11 base pairs

LEMOTH: 11 base pairs
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WEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATH:
PILING DATE: 09-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Bighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           other nucleic acid
                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100
Matches 11; Conservative
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STRANDEDNESS: single
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San Francisco
California
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                                                                                                94111-3834
                                                                     USA
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DESCRIPTION:
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US-08-838-545-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DESCRIPTION:
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US-08-838-545-44
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APPLICANT: Shay, Jerry W.
APPLICANT: Wright, Woodring E.
APPLICANT: Platyszek, Miezysław A.
APPLICANT: Orey, David R.
APPLICANT: Ore, David R.
APPLICANT: No. 6046307ton, James C.
TITLE OF INVENTION: Modulation of Mammalian Telomerase by
TITLE OF INVENTION: Peptide Nucleic Acids
                                 APPLICANT: Shay, Jerry W.
APPLICANT: Wright, Woodring E.
APPLICANT: Pieryszek, Mieczyslaw A.
APPLICANT: Corey, David R.
APPLICANT: No. 6046307cn, James C.
ATILE OF INVENTION: Modulation of Mammalian Telomerase by
TITLE OF INVENTION: Peptide Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 11; DB 3; Length 11; 100.0%; Pred. No. 1.6e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIF: 9411-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO COMPATIBLE
OPERATING SYSTEM: PC -DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURENT APPLICATION NUMBER: US/08/838,545
FILING DATE: 09-APR-1997
CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                                                           SSEE: Townsend and Townsend and Crew LL
T: Two Embarcadero Center, Eighth Floor
San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,019
FILING DATE: 09-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 31, Application US/08838545 Patent No. 6046307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Storella, John R. REGISTRATION NUMBER: 32,944 REFERENCE/DOCKET NUMBER: 01. TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 60 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTTAGGGTTAG 11
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                                                                                                                                                                                                                                                                                                                                                                                                                        California
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GENERAL INFORMATION:
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; Pred. No. 1.6e+02;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%;
Matches 11; Conservative 0;
                                                                                SEQUENCE CHARACTERISTICS:

LENGTH: 11 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MONECULE TYPE: RNA

US-08-998-443-2
                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GTTAGGGTTAG 11
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COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDTUM TYPE: FIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/98,443
FILING DATE: 05-JUN-1996
APPLICATION NUMBER: US/08/660,678
FILING DATE: 27-OCT-1994
PRIOR APPLICATION NUMBER: US/08/330,123
FILING DATE: 05-JUN-1996
APPLICATION NUMBER: US 08/330,123
FILING DATE: 07-OUT-1994
ATTONEY/AGENT INPORMATION:
NAME: SCOTELLA JOHN R:
REGISTRATION NUMBER: 32,944
REGISTRATION NUMBER: 32,944
REGISTRATION NUMBER: 32,944
REGISTRATION NUMBER: 32,944
REERRENCE/DOCKET NUMBER: 015389-000811US
TELECOMMUNICATION INFORMATION:
TELEFRAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DESULT 15

ESCULT 15

CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION WUMBER: US 08/630,019
FILING DATE: 09-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET WUMBER: 015389-001610US
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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/desc = "phosphorothioate (PS)
nucleic acid"
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Best Local Similarity
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MOLECULE TYPE: of DESCRIPTION: /
DES
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Sequence Sequence

AX268755 AX268759 AX104946 AX1104946 AX119567 BD085298 AX667174 AX668807 S50583 S50583 AX667174 AX668807 AX66807 AX668

AX268756 Sequence AX268758 Sequence

SUMMARIES

В

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gilchrest, B.A., Yaar, M. and Eller, M. Use of locally applied dna fragments Patent: WO 0174342-A 4 11-0CT-2001; PRUSTEES OF BOSTON UNIVERSITY (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4 from Patent W00174342.
AX268756
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synthetic construct
artificial sequences.
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Query
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AX269756/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
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                                                   December 31, 2003, 11:36:21; Search time 460.316 Seconds (without alignments) 444.364 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                       Gapop 10.0 , Gapext 1..v

Searched: 2888711 seqs, 20454813386 residues

Original number of hits satisfying chosen parameters:
Original DB seq length: 0
Naximum DB seq length: 30
Naximum Match 04
Maximum Match 1004
Listing first 45 summaries
                                    OM nucleic - nucleic search, using sw model
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117::
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                                                                                                   Sequence:
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AX268755 Sequence
AX268755 Sequence
AX104946 Sequence
AX104946 Sequence
AX119567 Sequence
AX119567 Sequence
AX667174 Sequence
AX66887 Sequence
AX66887 Sequence
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AX66897 Sequence
AX66891 Lype I proc
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AR107335 AR107344 AR123039 AR136787 AR160130 AR202278 AR217382 AR217382

AR241735 AR254391 AR287776

PAT 29-OCT-2001

linear

DNA

Pred. No. is the number of results predicted by chance to have a

ALIGNMENTS

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artificial sequences.

1 (bases 1 to 8)

Mcivor, R.S., Hackett, P. B. and Aguilar-Cordova, E.
Vector-mediated delivery of integrating transposon sequences
Patent: WO 0068399-A 6 16-NOV-2000;
REGENTS OF THE UNIVERSITY OF MINNESCTA (US); BAYLOR COLLEGE OF
MEDICINE (US); MCIVOR, R. Scott (US); Hackett, Perry B. (US);
Aguilar-Cordova, Estuardo (US)
Location/Qualifiers
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/organism="synthetic construct"
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/noTe="Direct Repeat Sequence"
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                                                                                              Mismatches
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                                            Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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/organism="synthetic construct"
/mol_type="genomic DNA"
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/organism="synthetic construct"
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/note="Synthetic DNA Fragment"
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/organism="synthetic construct"
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/db_xref="texcn:33630"
/note="Synthetic DNA Fragment"
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into DNA of a cell

Defent: JP 2001523450-A 10 27-NOV-2001;

REGENTS OF THE UNIVERSITY OF MINNESOTA

OS Artificial Sequence

PN JP 2001523450-A/10

PD 27-NOV-2001

PF 13-NOV-1997 US 60/065303

PR 13-NOV-1997 US 60/065303

PI PERRY B HACKETT, KARL J CLARK, ADAM J DAPIE, STEVEN C EKAR, PI

DAVID A LARLSEPAYDA, ZOLTAN IBYCUS, TSSUSANNA ISSUFARK PC

C12N15/09, A01K67/027, C07K16/18, C12N5/10, C12Q1/68, C12N15/00, PC

C12N15/00

CC Description of Artificial Sequence: A portion of a direct CC
B bp DNA linear PAT 27-AUG-2002 DNA-based transposon system for the introduction of nucleic acid into DNA of a cell.
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1 (Bacis Lo 8)
Hackett, P.B., Clark, K.J., Dapie, A.J., Ekar, S.C., Larjespayda, D.A.,
Ibycus, Z. and Issufark, T.
DNA-based transposon system for the introduction of nucleic acid
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Location/Qualifiers
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Location/Qualifiers
Lorganism="synthetic construct"
/mol type="genomic DNA"
/db_xref="taxon:32630"
/note="Synthetic DNA Fragment"
/ note="Synthetic DNA Fragment"
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JP 2001523450-A/10.
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                                                                                                                                                                                             PAT 30-APR-2001
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Krieg, A.M., Schetter, C. and Vollmer, J.C.
Immunostimulatory nucleic acids
Patent: WO 0122972-A 1138 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US); Coley Pharmaceutical
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1 (bases 1 to 8)
Messiaen.L. and Callens,T.
Improved mutation analysis of the nfl gene
Patent: WO 0129251-A 24 26-APR-2001;
UNIVERSITEIT GENT (BE)
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100.0%; Score 5; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels
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iive 0; Mismatches 0;
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Sequence 1138 from Patent WO0122972.
AX104946.1 GI:13921143
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Sequence 224 from Patent WO0129251.
AX119567
AX119567.1 GI:14036486
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon.9606"
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FRATURES GMDH (DE)

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1 (bases 1 to 9)
Truneyoshi, T., Westerhausen, A., Constantinou, C.D. and Prockop, D.J. Substitutions for glycine alpha 1-637 and glycine alpha 2-694 of type I procollagen in lethal osteogenesis imperfecta. The conformational strain on the triple helix introduced by a glycine substitution can be transmitted along the helix

9.1340689
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Position dependent recognition of gnn nucleotide triplets by zinc
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Location/Gualifiers
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type I procollagen [human, mRNA Mutant, 9 nt]
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/organism="synthetic construct"
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/db_xref="taxon:32630"....
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Patent: WO 0242459-A 2256 30-MAY-2002;
Sangamo Biosciences Inc. (US)
                                                                                   Sequence 2256 from Patent W00242459.
AX668807
AX668807.1 GI:29291782
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0 c 4 g 3 t
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3 c 2 g 3
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1. .9
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Position dependent recognition of gnn nucleotide triplets by zinc
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Position dependent recognition of gnn nucleotide triplets by zinc
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.0%; Pred. No. 4.5e+09; 0; Mismatches 0;
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Patent: WO 0242459-A 2220 30-MAY-2002;
Sangamo Biosciences Inc. (US)
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Patent: WO 0242459-A 623 30-MAY-2002,
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Sequence 2220 from Patent W00242459.
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Sequence 623 from Patent W00242459.
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synthetic construct
artificial sequences.

1 (bases 1 to 10)

Della Valle,F., Callegaro,L. and Negro,A.

Process for the preparation of genetic vectors for the nerve growth factor expression in eukaryotic cells
Patent: EP 0432510-A 12 19-UUN-1991;
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1 (bases 1 to 9)

1 Suneyoshi, T., Westerhausen, A., Constantinou, C.D. and Prockop, D.J. Substitutions for glycine alpha 1-637 and glycine alpha 2-694 of type I procollagen in lethal osteogenesis imperfecta. The conformational strain on the triple helix introduced by a glycine substitution can be transmitted along the helix
J. Biol. Chem. 266 (24), 15608-15613 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GenBank staff at the National Library of Medicine created this entry [NCBI glabbag 50885] from the original journal article. This sequence comes from Fig 5B.

Location/Qualifiers
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/organism="synthetic construct"
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type I procollagen (human, S50585
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:

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Result No.	Score	Query	Query Match Length DB	08	ID	Description	
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7	S	100.0	S	20	AA210696	Oligonucleotide se	
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۵	S	100.0	80	22	AAD02250	Direct repeat sequ	

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Gilchrest BA, Yaar M,

WPI; 1999-543520/46

A promoter regulat GAS complement gen	Cyclin D transcrip	Oligonucleotide se	Melanogenesis asso		finger pr	finger	finger	Donor oligomer wit	Merlin exon 14 spl	Oligonucleotide Ec	Anticancer duplex	Primer E19 for V.d	(dC-dA)n. (dG-dT)n	tag for	for		Yeast tag for NORF	Primer used in RAP	ner	p53 serial analysi	Chromophore contai	Ξ,	Human monocyte and	Human monocyte and	Oligonucleotide us	Oligonucleotide us	Mouse DNA adapter	Primer MR15 for mo	Human monocyte gen	Human macrophage g	ø	Human macrophage g	ø	ø	۵
AAV22350 AAV22283		AAZ10692							AAQ71104	•				_	•			·				AAC73931		-	-	•		•	AAA56166	AAA56218			AAA56321	AAA56331	
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22	1	2	ដ	2	ដ	ដ	ដ	ដ	ដ	10	2	5	ដ	ដ	2	2	2	5	2	2	2	2	2	2	2	2	5	2	2	2	2	2	2	ដ	5
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## ALIGNMENTS

p53 activity, UV mimetic, UV-irradiation, UV-induced dermatosis; UV-induced hyperproliferative disease; psoriasis; vitiligo; atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging; skin cancer, ss. Oligonucleotide sequence that increases p53 activity in a cell. AAZ10695 standard; DNA; 5 BP 99GB-0006758 98US-0048927 23-NOV-1999 (first entry) BOSTON 24-MAR-1999; 26-MAR-1998; (UYBO-) UNIV GB2336157-A. 13-OCT-1999 Synthetic. AAZ10695; AAZ10695/c 

DNA fragments useful for increasing p53 activity in a cell and reducing susceptibility to UV-induced hyperproliferative diseases -Claim 11; Page 30; 44pp; English

diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging and reducing susceptibility to skin cancer. activity in a cell. The oligonuclectides are are UV mimetics and protect cells against subsequent exposure to UV-irradiation or chemicals. The oligonuclectides are useful for increasing p53 activity in a cell, reducing the susceptibility to UV induced hyperproliferative AAZ10692-97 represent DNA fragments that are used for increasing p53

Sequence 5 BP; 1 A; 0 C; 2 G; 2 T; 0 other;

Gaps ó Length 5; 0; Indels 100.0%; Score 5; DB 20; L 100.0%; Pred. No. 5.2e+08; tive 0; Mismatches 0; Conservative Local Similarity les 5, Conserv

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CATAC 5

CATAC 1

AAZ10696 standard; DNA; 5 BP.

(first entry) 23-NOV-1999

Oligonucleotide sequence that increases p53 activity in a cell.

p53 activity, UV mimetic, UV-irradiation, UV-induced dermatosis, UV-induced hyperproliferative disease, psoriasis, vitiligo, atopic dermatitis, allergic rhinitis, conjunctivitis, photoaging, skin cancer; ss.

Synthetic.

GB2336157-A.

13-OCT-1999

Claim 1; Page 36; 74pp; English.

99GB-0006758 24-MAR-1999; 98US-0048927. 26-MAR-1998;

(UYBO-) UNIV BOSTON

Eller M; Yaar M, Gilchrest BA,

WPI; 1999-543520/46.

The invention describes inhibition of mammalian epithelial cell
proliferation by treating cells with at least one oligonucleotide, or
its fragment. The compounds, which have cytostatic, anti-allergic,
anti-inflammatory, dermatological, ophthalmological, anti-apsoriatic and
immunosuppressive activities, function as 'ultra-violet mimics' to induce
the constant processes (or a protective response to later exposure to
radiation or chemicals), as a proliferation inhibitor, apoptosis inducer
or a tumour necrosis factor inhibitor. Probably they mimic products of
DNA damage, or processed DNA-damage intermediates, by inducing the p53
pathway, resulting in transient arrest of cell growth, allowing more time
for DNA repair to occur before cell division takes place. The method is
especially used to treat carcinoma but may also be used to: treat other
typerproliferative states (e.g. psoriasis or precancerous conditions);
reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
allergically mediated inflammation (atopic or contact dermatitis,
allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in
cells caused by radiation or chemicals; increase melanin production
(pigmentation) in epithelial cells (e.g. for treating varialing), and to
promote apoptosis in epithelial cells that contain damaged DNA, Also

oligonucleotides that contain non-hydrolyzable backbones are used to inhibit apoptosis, in response to DNA damage, in epithelial cell. This sequence is melanogenesis associated oligonucleotide #4, a truncated version of the oligonucleotide shown in AAS14906, one of the oligonucleotides shown in AAS14916 into eithe proliferation, described in the method of the invention.

diseases, treating psoriasis, vitiligo, atopic dermatifis, allergic rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging and reducing susceptibility to skin cancer. AAZ10692-97 represent DNA fragments that are used for increasing p53 activity in a cell. The oligonucleotides are are UV minetics and protect cells against subsequent exposure to UV.irradiation or chemicals. The oligonucleotides are useful for increasing p53 activity in a cell, reducing the susceptibility to UV-induced hyperproliferative DNA fragments useful for increasing p53 activity in a cell and reducing susceptibility to UV-induced hyperproliferative diseases -Claim 11; Page 30; 44pp; English Ouery Match

Matches 5;

Matches 6;

Match

Sequence 5 BP; 2 A; 2 C; 0 G; 1 T; 0 other;

Query Match

100.0%; Score 5; DB 20; Length 5;

ö Melanin, melanogenic; oligomer; cytostatic; anti-allergic; p53; anti-inflammatory; dermatological; ophthalmological; anti-psoriatic; amunuosuppressive; DNA repair; proliferation inhibitor; apoptosis; tumour necrosis factor inhibitor; photoaging; hyperproliferative disease; carcinoma; oxidative stress; skin cancer; allergy mediated inflammation; conjunctivitis; allergic rhinitis; vitiligo; ss. Inhibiting proliferation of epithelial cells, useful e.g. for treating carcinoma, using specific oligonucleotides that mimic the effects of ultra-violet light Gaps ö Indels 5.2e+08; hes 0; Melanogenesis associated oligonucleotide #4. Mismatches 100.0%; Pred. ive 0; Mism Eller M; AAS14908 standard; DNA; 5 BP. 30-MAR-2001; 2001WO-US10162. 31-MAR-2000; 2000US-0540843. (first entry) Similarity 100 5; Conservative Gilchrest BA, Yaar M, WPI; 2001-626338/72. (UYBO-) UNIV BOSTON Ŋ 1 CATAC WO200174342-A2. 14-FEB-2002 .1-OCT-2001. Synthetic. AAS14908; Best Local Matches AAS14908/c RESULT 3 ઠે

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described in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention describes inhibition of mammalian epithelial cell trafferation by treating cells with at least one oligonuclectide, or proliferation by treating cells with at least one oligonuclectide, or its fragment. The compounds, which have cytostatic, anti-allergic, anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and immunosuppressive activities, function as 'ultra-violet mimics' to induce company processes (or a protective response to later exposure to radiation or chemicals), as a proliferation inhibitor, apoptossis inducer or a tumour necrosis factor inhibitor. Probably they mimic products of DNA damage, or processed DNA-damage intermediates, by inducing the p53 pathway, resulting in translent arrest of cell growth, allowing more time for DNA repair to occur before cell division takes place. The method is especially used to treat carcinoma but may also be used to: treat other of or DNA repair to occur before cell division takes place. The method is especially mediated inflammation (atopic or contact dermatitis, reduce photoaging, oxidative stress or damage; prevent skin cancer; treat allergically mediated inflammation (atopic or contact dermatitis, allergically mediated inflammation (atopic or contact dermatitis, allergic rhinitis and conjunctivitie); prevent or reduce DNA damage in cells caused by radiation or chemicals; increase melanin production (pigmentation) in epithelial cells that contain damaged DNA. Also coligonucleotides that contain non-hydrolyzable backbones are used to inhibit apoptosis, in response to DNA damage, in epithelial cells cellibulial cell proliferation, cinhibit mammalian epithelial cell proliferation,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53; anti-inflammatory; dermatological; ophthalmological; anti-psoriatic; immunosuppressive; DNA repair; proliferation inhibitor; apoptosis; tumour necrosis factor inhibitor; photoaging; hyperproliferative disease; carcinoma; oxidative stress; skin cancer; allergy mediated inflammation; conjunctivitis; allergic rhinitis; vitiligo; ss.
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                                                        100.0%; Score 5; DB 23; Length 5; 100.0%; Pred. No. 5.2e+08;
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Sequence 5 BP; 1 A; 0 C; 2 G; 2 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA fragments useful for increasing \mathfrak{p}53 activity in a cell and reducing susceptibility to UV-induced hyperproliferative diseases -
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5.2e+08;
Sequence 5 BP; 2 A; 2 C; 0 G; 1 T; 0 other;
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ive 0; Mismatches
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AAS14907 standard; DNA; 7 BP.
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Best Local Similarity 100.
Matches 5; Conservative
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anti-inflammatory; dermatological; ophthalmological; anti-psoriatic; anti-inflammatory; dermatological; ophthalmological; anti-psoriatic; immunosuppressive; DNA repair; proliferation inhibitor; apoptosis; tumour necrosis factor inhibitor; photoaging; hyperproliferative disease; carcinoma; oxidative stress; skin cancer; allergy mediated inflammation; conjunctivitis; allergic rhinitis; vitiligo; ss.
                                                                                                                                                                Melanogenesis associated oligonucleotide #3.
                                                                              (first entry)
                                                                                  14-FEB-2002
AAS14907
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Synthetic.

WO200174342-A2

11-OCT-2001

30-MAR-2001; 2001WO-US10162

31-MAR-2000; 2000US-0540843

(UYBO-) UNIV BOSTON.

Eller M; Yaar M, Gilchrest BA,

WPI; 2001-626338/72

Inhibiting proliferation of epithelial cells, useful e.g. for treating carcinoma, using specific oligonucleotides that mimic the effects of ultra-violet light

Claim 1; Page 36; 74pp; English.

The invention describes inhibition of mammalian epithelial cell proliferation by treating cells with at least one oligonucleotide, or its fragment. The compounds, which have cytostatic, anti-inflammatory, dermatological, ophthalmological, anti-ipsoriatic and immunosuppressive activities, function as 'ultra-violet mimics' to induce DNA repair processes (or a protective response to later exposure to radiation or chemicals), as a proliferation inhibitor, apoptosis inducer or a tumour necrosis factor inhibitor. Probably they mimic products of DNA damage, or processed DNA-damage intermediates, by inducing the p53 pathway, resulting in transient arrest of cell growth, allowing more time for DNA repair to occur before cell division takes place. The method is especially used to treat carcinoma but may also be used to: treat other hyperproliferative states (e.g., psoriasis or precancerous conditions); reduce photoaging, oxidative stress or damage; prevent skin cancer; treat allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in cells caused by radiation or chemicals; increase melanin production (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to promote apoptosis in epithelial cells that contain damaged DNA. Also oligonuclectides that contain non-hydrolyzable backbones are used to inhibit apoptosis, in response to DNA damage, in epithelial cell. This sequence is melanogenesis associated oligonuclectide #3, a truncated version of the oligonuclectide shown in AAS14906, one of the oligonuclectides used to inhibit mammalian epithelial cell proliferation, described in the method of the invention.

Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 other;

Gaps .. 100.0%; Score 5; DB 23; Length 7; Similarity 100.0%; Pred. No. 3.7e+08; 5; Conservative 0; Mismatches 0; Indels Query Match Best Local Similarity Matches

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AAS14911/c ID AAS14911 standard; DNA; 7 BP.

AAS14911;

(first entry) 14-FEB-2002

Melanogenesis associated oligonucleotide #7.

Melanin, melanogenic; oligomer; cytostatic; anti-allergic; p53; anti-inflammatory; dermatological; ophthalmological; anti-psoriatic; ammunosuppressive; DNA repair; proliferation inhibitor; apoptosis; tumour necrosis factor inhibitor; photoaging; hyperproliferative disease; carcinoma; oxidative stress; skin cancer; allergy mediated inflammation; conjunctivitis; allergic rhinitis; vitiligo; ss:

Synthetic.

Location/Qualifiers /\*tag= a /mod base= modified\_base

/mod\_base= a /note= "Phosphorylated"

11-OCT-2001.

WO200174342-A2

30-MAR-2001; 2001WO-US10162.

31-MAR-2000; 2000US-0540843

(UYBO-) UNIV BOSTON

Eller M; Gilchrest BA, Yaar M,

WPI; 2001-626338/72

Inhibiting proliferation of epithelial cells, useful e.g. for treating carcinoma, using specific oligonucleotides that mimic the effects of ultra-violet light

Claim 1; Page 38; 74pp; English.

tragment. The compounds, which at least one oligoniclectide, or its fragment. The compounds, which have cytostatic, anti-postratic and anti-inflammantory, dermatological, ophthalmological, anti-postratic and immunosuppressive activities, function as "ultra-violet mimics' to induce DNA repair processes (or a protective response to later exposure to radiation or chemicals), as a proliferation inhibitor, apoptosis inducer or a tumour necrosis factor inhibitor. Probably they mimic products of DNA damage, or processed DNA-damage intermediates, by inducing the p53 pathway, resulting in transient arrest of cell growth, allowing more time (for DNA repair to occur before cell division takes place. The method is especially used to treat carcinoma but may also be used to: treat other hyperproliferative strates (e.g. psoriasis or precancerous conditions); reduce photoaging, oxidative stress or damage; prevent skin cancer; treat allergically mediated inflammation (atopic or contact dermatitis, allergic rhintis and conjunctivitis); prevent or reduce DNA damage in caused by radiation or chemicals; increase melanin production ackbones are used to epithelial cell. This (pigmentation) in epithelial cells (e.g. for treating vitiligo), and promote apoptosis in epithelial cells that contain damaged DNA. Also oligomucleotides that contain non-hydrolyzable backbones are used to inhibit apoptosis, in response to DNA damage, in epithelial cell. Thi sequence is melanogenesis associated oligonucleotide #7, one of the oligonucleotides used to inhibit mammalian epithelial cell proliferation, described in the method of the invention. The invention describes inhibition of mammalian epithelial 

Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 other;

Length 7; Score 5; DB 23; I Pred. No. 3.7e+08; 100.0%; 100.0%; Best Local Similarity Query Match

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Matches

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The present sequence represents a promoter regulatory element, found in the utrons of the invention. Utrons are from, or are homologous to, the 3' untranslated region (UTR), of an mRNA that stimulates or inhibits a cellular response by sequence specific interactions. The utron is able to suppress constitutive and interferon-gamma (IFN-gamma) induced major histocompatibility complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (WHC) class I and class II antigen expression and expression of other antigens, the gene promoters of which contain related sequence motifs that are stimulated by the same factors which stimulate MHC class I are class II antigen expression. Such utrons can be used to regulate species on in a subject, e.g. a human or a cell in vitro, specifically inhibiting MHC class I or II. ICAM-7, B7-1, B7-2, RC gamma R, II-2 or HIV gene expression. They can be used to inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ransplant rejection, or treat an autoimmune or inflammatory disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Utrons, RNA molecules containing promoter regulatory motifs -useful to suppress express expression from promoter of interest, specifically TSU nucleic acid suppression of MHC Class I and II gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                 3' untranslated region, UTR; inhibition, gene expression; ICAM-7; interferon-gamma; IRN-gamma; major histocompatibility complex; MHC; antigen expression; gene promoter; urron; B7-1; B7-2; Fc gamma R; HIV gene expression; transplant rejection; treatment; autoimmune disease; inflammatory disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                        A promoter regulatory motif found in the utrons of the invention.
    Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 9;
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100.0%; Pred. No. 2.9e+08;
ive 0; Mismatches 0;
                          3.2e+08;
    DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9 BP; 3 A; 0 C; 3 G; 3 U; 0 other;
                                                   0; Mismatches
    100.0%; Score 5; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; Page 20; 200pp; English.
                                                                                                                                                                                                                                                              AAV22350 standard; RNA; 9 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97WO-US09459
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                                                   Conservative
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Best Local Similarity
Matches 5; Conserv
    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified.
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                                                                                                                                                                                                                                                                                                                                                           29-JUN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression
                                                                                                                                                                                                                                                                                                             AAV22350;
                                                                                                                                                                                                                                           AAV22350/c
                          Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The patent discloses non-integrating viral vectors comprising a polynucleotide flanked by inverted repeats that bind a transposase, a transposase-encoding polynucleotide operably linked to a regulatory sequence comprising an operator, that alters expression of the transposase-encoding polynucleotide. Transposon sequences can integrate into genomic DNA whether or not the cell is dividing. Ad8810 is a SB (Sleeping Beauty) transposase-transducing adenoviral non-integrating vector. The non-integrating viral vectors are useful for treating to append to disease characterised by subnormal production of a polypeptide or RNA, e.g. for replacement of a defective gene, delivery of a polypeptide dang or supplementation of a metabolic activity. These genetic diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    include cyefic fibrosis, diabetes, cardiovascular disease, cancer or brain malfunction. The non-integrating viral vectors are useful as mucleic acid delivery systems, e.g. for genome analysis or gene therapy and can also be used for applications that involve long-term production of a polypeptide. The non-integrating viral vectors are also useful for creating transgenic host cells that provide normal cells with protection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Non-integrating (adenovirus-based) viral vectors useful in gene therapy, especially for creating patients suffering from a genetic disease, e.g. cystic fibrosis, diabetes, cardiovascular disease, cancer or brain malfunction
                                                                                                                                                                                                                                                                                                                                                                                                                           non-integrating viral vector; cytostatic; anti-diabetic; cardiant; neuroprotective; genetic disease; gene therapy; therapy; cancer; cystic fibrosis; diabetes; cardiovascular disease; brain malfunction; genome analysis; chemotherapy; transgenic host cell; direct repeat; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence of the present invention is a direct repeat sequence that binds to SB protein.
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  Indels
                                                                                                                                                                                                                                                                                                                                                                                                     AdSB10; adenovirus; transposase;
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                                                                                                                                                                                                                                                                                                                                                    Direct repeat sequence that binds to SB protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8 BP; 4 A; 3 C; 0 G; 1 T; 0 other;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mcivor RS, Hackett PB, Aguilar-Cordova
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 14; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BAYLOR COLLEGE MEDICINE. MCIVOR R S.
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                                                                                                                                                                                                             AAD02250 standard; DNA; 8 BP.
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                                                                                                                                                                                                                                                                                                        (first entry)
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MINU ) UNIV MINNESOTA
                                                                                                                                                                                                                                                                                                                                                                                                        Sleeping Beauty; SB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-024870/03.
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                                            CATAC 5
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(HACK/)
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Gaps

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AAV22283;

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WPI; 1998-018505/02.
                                                    (UYYA ) UNIV YALE.
                                Unidentified
                                            21-MAY-1997;
                                                21-MAY-1996;
                                    WO9744450-A1
                                        27-NOV-1997.
                                                        Peyman JA;
                                                                      expression
                                                                                                                       Query Match
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This is a nonamer consensus sequence of a cyclin D transcription factor

DMP1. DMP1 is an amino acid polymer which has binding affinity for a
D-type cyclin, in vitro, and for a specific DM nucleotide sequence and
is a transcription factor involved in the activation of genes that
prevent cell proliferation. The DMP1 nucleic acid is operatively linked
con an expression control sequence in an expression vector. The expression
vector has a transcription control sequence comprising this nonamer
sequence operably associated with a recombinant gene or a cassette
insertion site for a recombinant gene. The vector is homologously
recombined in a chromosome of a transgenic animal. A probe or a
competitor in DMP1 transactivation assays is designed based on this
competitor in DMP1 transactivation assays is designed based on this
confidence. The presence of activity of DMP1 can be determined by
detecting binding of DMP1 and a probe by contacting a biological sample
from a mammal with the probe under conditions that allow binding of the
type presence or activity of DMP1 is suspected in the sample. DMP1 can
chuction as a cell cycle inhibitor when expressed in a tumour cell.
Modulating the expression of DMP1 can be used to treat tumours and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancers. DMP1 can also be used for controlling expression of heterologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteins. Antisense sequences and ribozymes can be used to inhibit expression of the transcription factor. Detecting the level and activity of DMP1 in cells is useful for detection of cancer cells or
                                                                                                                                                                                                                                            cyclin D transcription factor; binding affinity; D-type cyclin; probe; cell cycle inhibitor; tumour; detection; cancer; DMP1; competitor;
                                                                                                                                                                                              Cyclin D transcription factor DMP1 nonamer consensus sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cyclin D transcription factor and related DNA develop products for treatment of, e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 99; 120pp; English
                                                                                                                                                                                                                                                                                                          nonamer consensus sequence; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hirai H, Inoue K, Sherr CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0017815.
96US-0017815.
96US-0648837.
                            AAV15899 standard; DNA; 9 BP.
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                                                                                                                                        (first entry)
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5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-008884/01
                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9743415-A1
                                                                                                                                        26-MAY-1998
                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-MAY-1997;
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Best Local S:
Matches 5,
                                                                                  AAV15899;
AAV15899/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a GAS complement gene promoter motif found in a trophoblast STAT utron (TSU) TSUB be isolated from a CDNA library prepared from mRNA isolated from trophoblast cells. Utrons are from, or are homologous to, the 3' untranslated region (UTR), of an mRNA that stimulates or inhibits a cellular response by sequence specific interactions. The TSU is able to suppress constitutive and interferon-gamma (IFN-gamma) induced major histocompatibility complex (MHC) class I and class II antigen expression and expression of other antigens, the gene promoters of which contain related sequence motifs that are stimulated by the same factors which stimulate MHC class I and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    class II antigen expression. The TSU sequence contains motifs related to thrw signalling (OGAS, ISRE and interleukth-4 response elements). The nucleic acid can be used to requiate gene expression in a subject, e.g. a human or a cell in vitro, specifically inhibiting MHC Class I or II,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ICAM-7, B7-1, B7-2, FC gamma R, IL-2 or HIV gene expression. It can be used to inhibit transplant rejection, or treat an autoimmune or inflammatory disease or disorder. It can also be used to inhibit the
                                                                                                                                                                                                                                                                                                                           Trophoblast STAT utron, TSU, 3' untranslated region, UTR; inhibition, interferon-gamma, IFN-gamma; major histocompatibility complex; MHC; antigen expression; gene promoter; class I; class II; IFN signalling; GAS; ISRE; interleukin-4 response element; gene expression; ICAM-7; B7-2; Fc gamma R; HIV gene expression; transplant rejection; treatment; autoimmune disease; inflammatory disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                              GAS complement gene promoter motif found in a trophoblast STAT utron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Utrons, RNA molecules containing promoter regulatory motifs useful to suppress express expression from promoter of interest, specifically TSU nucleic acid suppression of MHC Class I and II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 22; Page 90; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   action of STAT1-6, or a cytokine.
                                                                                                               AAV22283 standard; DNA; 9 BP
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                              100.0%; Score 5; DB 19; Length 9; 100.0%; Pred. No. 2.9e+08; ive 0; Mismatches 0; Indels
Sequence 9 BP; 1 A; 3 C; 2 G; 3 T; 0 other;
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RESULT 12

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RESULT 11

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Query Match
Best Local Similarity 100.
                                   WPI; 1999-543520/46.
                       (UYBO-) UNIV BOSTON
            24-MAR-1999;
                  26-MAR-1998;
GB2336157-A.
      13-OCT-1999
9/2004^{\circ}
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The invention describes inhibition of mammalian epithelial cell

proliferation by treating cells with at least one oligonucleotide, or

its fragment. The compounds, which have cytostatic, anti-apsoriatic and

anti-inflammatory, dermatological, ophthalmological, anti-apsoriatic and

immunosuppressive activities, function as 'ultra-violet mimics' to induce

containing or chemicals', as a proliferation inhibitor, apoptosis inducer

contatumour necrosis factor inhibitor. Probably they mimic products of

DNA damage, or processed DNA-damage intermediates, by inducing the p53

containing or processed DNA-damage intermediates, by inducing the p53

containing or processed DNA-damage intermediates, by inducing the p53

containing or transient arrest of cell growth, allowing more time

for DNA repair to occur before cell division takes place. The method is

contained to treat carcinoma but may also be used to: treat other

containing to treat carcinoma but may also be used to: treat other

contained inflammation (atopic or contact dermatitis,

allergically mediated inflammation (atopic or contact dermatitis,

allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in

colls caused by radiation or chemicals; increase melanin production

(pigmentation) in epithelial cells that contain damaged DNA. Also

conjequence apoptosis in response to DNA damage, in epithelial cells

conjequence is melanogenesis associated oligonucleotide #1, one of the

colls production or chemicals, in epithelial cells

conjequence is melanogenesis associated oligonucleotide #1, one of the

colls contained to inhibit mammalian epithelial cell

conjequence is melanogenesis associated oligonucleotide #1, one of the

colls production or contain damages in epithelial cells

colls production or contain damages to DNA damage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inhibiting proliferation of epithelial cells, useful e.g. for treating carcinoma, using specific oligonucleotides that mimic the effects of ultra-violet light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oligonucleotides used to inhibit mammalian epithelial ce
proliferation, described in the method of the invention
                                                                                                           /mod_base= g
/note= "Optionally phosphorylated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9 BP; 3 A; 0 C; 4 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 36; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                          Yaar M, Eller M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABX03786 standard; DNA; 9 BP
                                                                                                                                                                                                                                                                           30-MAR-2001; 2001WO-US10162.
                                                                                                                                                                                                                                                                                                                             31-MAR-2000; 2000US-0540843
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                                                                                  /*tag=
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modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ10692-97 represent DNA fragments that are used for increasing p53 activity in a cell. The oligonucleotides are are UV minetics and protect cells against subsequent exposure to UV-irradiation or chemicals. The oligonucleotides are useful for increasing p53 activity in a cell, reducing the susceptibility to UV-induced hyperproliferative diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic rhintis, conjunctivitis, and UV-induced dermatoses, reducing photoaging and reducing susceptibility to skin cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA fragments useful for increasing p53 activity in a cell and reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                       p53 activity, UV mimetic, UV-irradiation, UV-induced dermatosis, UV-induced hyperproliferative disease, psoriasis, vitiligo, atopic dermatitis, allergic rhinitis, conjunctivitis, photoaging, skin cancer; ss.
                                                                                                                                                                            Oligonucleotide sequence that increases p53 activity in a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               susceptibility to UV-induced hyperproliferative diseases
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100.0%; Pred. No. 2.9e+08;
tive 0; Mismatches 0;
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AAS14905 standard; DNA; 9 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99GB-0006758.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gilchrest BA, Yaar M,
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Gaps ö

Synthetic

AAS14905;

RESULT 13 AAS14905,

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The invention relates to a differential display comprising contacting cDNA with a first primer that hybridies to an oligonucleic sequence coding for a leucine-rich motif, and with a second oligonucleotide primer to form a cDNA-hybrid molecule. The method comprises obtaining mRNA from at least 2 samples, synthesising CDNA from the RNA of each sample, contacting the cDNA with a first primer that hybridises to an oligonucleic sequence coding for a leucine-rich motif, and with a second oligonucleotide primer to form cDNA-hybrid molecules, detecting amplified products and comparing the amplified products from each sample to identify distinctive amplified products coding for at least one secreted or transmembrane protein. The method is useful for discovering novel secreted and/or transmembrane proteins which are important for cell processes and play an important role in determining its phenotype, and which act as mediators for the transfer of signals from external environment into the cell itself, thus modulating gene expression. Sequences ABX03772-ABX03790 represent PCR primers used in the differential display method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Differential display method for identifying secreted or transmembrane protein, comprises contacting a DNA with a first primer that hybridizes to a sequence coding for a leucine-rich motif and with a second oligonucleotide primer -
Differential display method; leucine-rich motif; transmembrane protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
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                                                      secreted protein; primer; PCR; ss; human.
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Matches 5; Conservative
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KW Differenti
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KW SCOOSS925
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KW D1-AUG-200
KW D1-AUG-200
KW Z3-JAN-200
KW Z3-JAN-Z00
KW 
                                                                                                                                                                                     Synthetic
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The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (F1), a second (F2), and a third (F3) can described site, comprising a first (F1), a second (F2), and a third (F3) target site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (I) a polypeptide (II) designing (I); (2) a polynucleotide (III) encoding (I) or (III); and (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, selecting the F2 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target subsites having the nucleotide G in the 5'-most position of the subsite. (I) is useful in studying gene function, and for human the engineering (I), (II) or (III) is useful in a subject, in diagnostic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determined the carget nucleic acid in a sample, and an assays to determined the carget nucleic acid in a sample, and an assays to secuence affinity and specificity for their target sequences, as well as enhanced biological activity. ABG71213 to ABG72214 and ABP48191 to ABP51230 the properties of the proper
                                                                                                                                                                                                                                                                                                                                                New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to
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100.0%; Pred. No. 2.9e+08;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 45; 81pp; English
                                                                                                                                                                         (SANG-) SANGAMO BIOSCIENCES INC.
                                                                                                                20-NOV-2000; 2000US-0716637.
                                                         20-NOV-2001; 2001WO-US43438
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: 145.494 secs

Job time

Zinc finger protein related oligonucleotide target SEQ ID NO:623.

ABQ71504 standard; DNA; 9 BP.

28-AUG-2002 (first entry)

Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.

WO200242459-A2

Homo sapiens

Synthetic

Gaps

; 0

0; Indels

100.0%; Score 5; DB 24; Length 9; 100.0%; Pred. No. 2.9e+08;

0; Mismatches

1 CATAC 5 CATAC 5 us-09-540-843-6.szlm30.rst

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C21103 HUMGS000262
BM397954 5009-0-39
AA977115 0624508.8
A1120725 ub72b11.r
A177751 u121h05.x
C00646 HUMGS000819
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AZ46490 INOZ7GZI
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Tetrahymena thermophila cDNA, mRNA sequence.
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5.J. and Klobutcher, L.

6.J. from Tetrahymena thermophila, strain CU428.1, growing cells Unpublished
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
University of Chicago
920 E. Seth Street, Chicago, IL 60637, USA
                    BQ595683 E012692-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BST.
Tetrahymena thermophila
Tetrahymena thermophila
Bukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
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AZ4515195
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AZ424551
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 BM398220 5009-0-42
AI424037 tf51h06.x
AI685758 tu37g09.x
AI721735 fc31g08.x
                                                                 ; Search time 574.494 Seconds (without alignments) 211.530 Million cell updates/sec
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       GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                         Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Trocal number of hits satisfying chosen parameters:

Raximum DB seq length: 0

Raximum DB seq length: 30

Sost-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;, mRNA sequence.
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AI685758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bonaldo, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: WCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                  db xref="taxon:5911" /clone lib="Chilcoat/Turkewitz cDNA (large fraction)" /note="Vector: BlueScript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleogtomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 16)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological bisorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                         Proc. Natl. Acad. Sci USA, 98: 8709-8713."
5 c 0 g 5 t
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lab host="DH108"
organism="Tetrahymena thermophila"
                                                                                                                                                                                                                                                                                                                           100.0%; Score 5; DB 12; L
100.0%; Pred. No. 1.8e+06;
ive 0; Mismatches 0;
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/organism="Homo sapiens"
/mol_type="mRNA"
/db xref="taxon:9606"
/clone="IMAGE:2102843"
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9
                           /mol_type="mRNA"
/strain="CU428.1"
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Homo sapiens
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Best Local Similarity
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COMMENT
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05/19/2004

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/AGLOBEL INTERPORT CGAP Pr28"

//Clone lib="NCI CGAP Pr28"

//Tote="Organ: prostate; Vector: pT773D-Pac (Pharmacia)

with a modified polylinker; Plasmid DNA from the modified library NCI CGAP Pr22 was prepared, and secircles were made in vitro. Following HAP purification, reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 985608-986759, 1101192-1101959, and 1217928-1220615).

Subtraction by Bento Soares and M. Fatima Bonaldo. "a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapDs-remail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Bumert-Buck, M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Mashington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 16)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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100.0%; Score 5; DB 9; Length 16; 100.0%; Pred. No. 1.8e+06;
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Seg primer: -400P from Gibco
High quality sequence stop: 1.
Location/Qualifiers
                                                                 0; Mismatches
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
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/db_xref="taxon:9606"
/clone="IMAGE:2253280"
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/lab_host="DH10B"
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BG929060 17 bp mRNA linear EST 06-NOV-2001
HNC11-1-G8.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo.
I (bases 1 to 16)
Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     onancomithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay_kumar-1@gsk.com
                                                                                                                                                                                                                                                                                                                        BG928185 16 bp mRNA linear EST 06-NOV-HNC65-1-D12.R.R HNC (Human Normal Cartilage) Homo sapiens cDNA,
                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identification and initial characterization of 5000 expressed sequenced tags (BSTs) each from adult human normal and osteoarchritic cartilage cDNA libraries Osteoarchritic actilage cDNA libraries Osteoarchr. Cartil. 9 (7), 641-653 (2001)
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/db_xref="taxon:9606"
/tiseue_type="cartilage"
/clone lib="HNC (Human Normal Cartilage)"
/note="Vector: pSPORT I; Site_1: Sall; Site_2: Not!;
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                                100.0%; Score 5; DB 9; Le Similarity 100.0%; Pred. No. 1.8e+06; 5; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 1.8e+06;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
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Matches 5; Conserv
                                Query Match
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DEFINITION
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BG928185
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KEYWORDS
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BG929060
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                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 16)
Clark, M. Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S.L., Hillier, L., Walaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
                                                         EST 07-JUN-2001
                              16 bp mRNA linear EST 07-JUN-200: fc31g08.x1 Zebrafish WashU MPING EST Danio rerio cDNA clone IMAGE:3723038 3' similar to SW:YM14_PARTE P15615 HYPOTHETICAL 47.2 A17317316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: zbrafish@watson.wustl.edu
cDNA Library Preparation: Matthew Clark. CDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
Info@genomesystems.com) and Research Genetics, Hustsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: T7 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WashU Zebrafish EST Project 1998
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Danio rerio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:3723038"
                                                                                                                                                                                                                                      Danio rerio (zebrafish)
                                                                                                                                                                                       AI721735.1 GI:5040064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             www.rzpd.de)
                                                                                                                                                                                                                                                                 Danio rerio
                                                                                                                                                    ACCESSION
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                                                                               DEFINITION
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RESULT 4
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05719/2004
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project

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Gaps

us-09-540-843-6.szlm30.rst

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/clone lib="MPIZ-ADIS-024-developing root"
/folome lib="Wetcor: pCMVSPORT6; Site 1: Sal1; Site 2: Not1;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Binbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sal1-Not1, primer sites and
                               mol type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C21103 17 bp mRNA linear EST 31-DEC-2002 HUMGS0002626 Human adult (K.Okubo) Homo sapiens cDNA 3', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SP6-Sall-CCACGCGTCCG-Sprime-cDNA-polyA-CC-Not1-T7; Note:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 17)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Institute for Molecular and Cellular Biol
Osaka University
1-3, Yamada-oka, Suita, Osaka Pref. 565, Japan
1-1, Yamada-oka, Suita, Osaka Pref. 565, Japan
1-1, Osaka-Oka, Suita, Osaka-u.ac.jp
Me are not submitting the same cDNA sequence redundantly to DDBJ We are not submitting the same cDNA sequence redundantly to BBJ Sequence in this library and as well as in other 3'-directed libraries, see 'http://www.imcb.osaka- u.ac.jp/bodymap'. The sequences of the clones represented by this GS sequences is also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing granted in the context of the GABI-Beet proj
, local PI: Dr. Katharina Schneider, coordinator: Prof.
Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
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/organism="Homo sapiens"
/mol_type="mRNA"
/db xref="taxon:9606"
/dev_stage="adult"
/clone lib="Human adult (K.Okubo)"
/note="One or more human adult tissue"
5 c 2 g 5 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                         /db_xref="GABI:191174"
/db_xref="taxon:161934"
/dbone="034-022-H17"
/tissue_type="developing root"
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      'organism="Beta vulgaris"
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100.0%;
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5; Conserv
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1 (bases 1 to 17)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., and Radelof,U., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
                                                                   Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
Contact: Weisshaar B
                                                                                                                                                                                                                                                                                                                                                                                                                                  GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI; Directional"
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// Organism="Homo sapiens"
// Organism="Homo sapiens"
// Ob_xref="taxon:9606"
// Ob_xref="taxon:9606"
// Issue_Eype="cartilage"
// Iab_host="E.coli DH10 B"
// Clone_lib="HNC (Human_Normal_Cartilage)"
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Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Pax: 00492215062851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 17 Std Error: 0.00
Plate: 22 row: H column: 17
Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax: 610-270-5598
Email: Banjay kumar-1@gsk.com
Seq primer: T7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                           Contact: Sanjay Kumar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 610-270-7245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 610-270-1916

Tel: 610-270-1916

Email: sanjay
Seq primer: Locary
Seq primer: Seq 
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us-09-540-843-6.szlm30.rst

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Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
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Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E., Frankel
J. and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished
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/mol_type="mRNA"
fatrain="CU428.1"
/db xref="CU428.1"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: BlueScript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Hymenostomatida, Tetrahymenina; Tetrahymena.
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100.0%; Pred. No. 1.9e+06;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637,
Tel: 773 702 4374
Mismatches
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Email: apturkew@midway.uchicago.edu
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Email: cgapbs-r@mail.nih.gov
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Tetrahymena thermophila
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Homo sapiens
5; Conservative
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
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BM397954
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1. .19
| Organism="Homo sapiens"
| Mol_type="mRNA" |
| Mol_type="mRNA" |
| Ab xxef="taxon:9606" |
| Ab bost="INAGE:1587278" |
| Ab host="pooled germ cell tumors" |
| Ab host="Petcor: pr773D-pac (Pharmacia) with a modified |
| Anote="Vector: pr773D-pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pr773 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "

2 a 0 c 7 9 10 t
Emmert-Buck, M.D., Ph.D. cDN Library Preparation: M. Bento Soares, Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCT-CSp. clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musn.
1 (Dases 1 to 19)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Stepte, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 5; DB 9; Length 19; 100.0%; Pred. No. 1.9e+06;
                                                                                                                                                                                                                                                                                        Trace considered overall poor quality
Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
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The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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EST 31-DEC-2002
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 19)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Osaka University
1-3. Yamada-oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-511(ex.315)
Email: kousaku@imcb.osaka-u.ac.jp
Ma are not submitting the same cDNA sequence redundantly to DDBJ
since 1993. For the abundance information of clones with this
sequence in this library and as well as in other 3'-directed
libraries, see 'http://www.imcb.osaka-u.ac.jp/bodymap'. The
sequences of the clones represented by this GS sequences is also
found there.
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HUMGS0008192 Human adult (K.Okubo) Homo sapiens CDNA, mRNA
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/mol_type="mRNA"
/db_xref="texon:9606"
/dev_stage="adult"
/clone lib="Human adult (K.Okubo)"
/note="One or more human adult tissue"
                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 5; DB 9; Le
100.0%; Pred. No. 1.9e+06;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Institute for Molecular and Cellular Biol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BodyMap; human gene expression database
                 /dev_stage="embryo, 14 dpc"
/lab_host="DH108"
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/clone="IMAGE:2088249"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence.
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JOURNAL
COMMENT
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AUTHORS
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                                                                                                                                                                                                                    /Glone_lib="Soares mammary_gland_NMLMG" note="Vector: pr773b-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pr773 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. " a
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Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., The Washlo-NCI Mouse EST Project 1999
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AI747751 19 bp mRNA linear EST 22-3 ul21h05.x1 Sugano mouse embryo mewa mus musculus CDNA clone limAGE:2086249 3' similar to TR:P79101 P79101 CLEAVAGE AND POLYADENYLATION SPECIFITY FACTOR PROTEIN: ;, mRNA sequence.
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Possible reversed clone: similarity on wrong strand
Seq primer: custom primer used
High quality sequence stop: 1.
Location/Qualifiers
Possible reversed clone: similarity on wrong strand
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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100.0%; Pred. No. 1.9e+06;
iive 0; Mismatches 0;
               Seg primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                 /sex="female (lactating)"
/tissue_type="mammary gland"
/lab_host="DH108"
                                                                                        /organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
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                                                                                                                                                 clone="IMAGE:1383261"
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/strain="C57BL"
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Best Local Similarity
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Gaps

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gij 473214 glp hR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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84112, USA
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Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
'M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                                                                             A2345849 11082 19 bp DNA linear GSS 29-SEP-200 1M0080D16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0080D16 R, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 5; DB
100.0%; Pred. No. 1.9
:ive 0; Mismatches
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="UUGC1M0080D16"
/sex="Male"
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Location/Qualifiers
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Plate: 0080 row: D c
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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AUTHORS
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                                                                                                                                                                                                      AZ341880
1M0074004R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0074004 R, genomic survey sequence.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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Length: 10000 Std Error: 0.00
0074 row: O column: 04
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Seg primer: CACACAGGAAACAGCTATGACC
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University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0074004"
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Location/Qualifiers
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Fax: 801 585 7177
Email: ddunn@genet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Conservative
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Db 1 CATAC 5

Search completed: December 31, 2003, 19:41:24

Job time: 574.494 secs

Copied from 09980559 on 05/19/2004

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Sequence 20, Application US/08855372B
Patent No. 6090549
GENERAL INFORMATION:
APPLICANT: Mizzabekov, Andrei D
APPLICANT: Parinov, Sergei V
APPLICANT: Barsky, Victor E
APPLICANT: Kirillov, Eugene V
APPLICANT: Linilov, Sugene V
APPLICANT: Dubiley, Svetlana A
TITLE OF INVENTION: Use of Continuous/Contiguous Stacking Hybridization as a Diagno NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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31, Appl
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                                                          US-09-123-638-1
US-08-646-695-30
US-08-845-233-31
US-08-724-75-31
US-09-724-75-31
US-09-724-75-31
US-09-427-834A-34
US-09-427-834A-34
US-09-508-7538-252
US-09-508-7538-273
US-09-508-7538-273
US-09-508-7538-273
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US-09-508-7538-273
US-09-508-7538-273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADJUSTEE TO N. MACHER STREET SO N. MACHER STATE: 111inois COUNTRY: United States COMPUTRY: United States COMPUTER READABLE FORM:
MEDIUM TYPE: 3.50 inch, 1.4 MB storage
                       -09-063-450-24
-09-063-450-33
-09-123-638-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/855,372B
FILING DATE: 13-MAY-97
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/587,332
FILING DATE: 16-JAN-96
ATTORNEY/AGENT INFORMATION:
NAME: Cherskov, Michael J.
REGISTRATION NUMBER: 33,664
REFERENCE/DOCKET NUMBER: ANL-IN-95-027
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: No. 6090549 Applicable
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20 N. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (312) 621-1330
TELEFAX: (312) 621-038
INCORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomic DNA
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HYPOTHETICAL: yes
RESULT 1
US-08-855-372B-20/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-855-372B-20
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Sequence 3, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 8, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 6, Appli
Sequence 6, Appli
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Sequence 4, Appli
Sequence 20, Appl
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Appli
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Appl
                                                                                                                                                 December 31, 2003, 14:40:05 ; Search time 19.4304 Seconds (without alignments) 113.581 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 174,
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Sequence 1, A
Sequence 1, A
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Sequence
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(cgn2_6/ptodata/1/ina/5A_COMB.seq:*

(cgn2_6/ptodata/1/ina/5A_COMB.seq:*

(cgn2_6/ptodata/1/ina/6A_COMB.seq:*

(cgn2_6/ptodata/1/ina/6B_COMB.seq:*

(cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*

(cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
                  GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                Gapop 10.0, organization Gapop 10.0, organization S69978 seqs, 220691566 residues Frotal number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries
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US-08-468-609A-174
                                                                                                         nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Match Length
                                       Copyright
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                                                                                                                                                                                                                                         Title:
Perfect score:
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APPLICANT: FARRANCE, Iain K.G.
APPLICANT: HALL, Deborah B.
APPLICANT: STEWART, Alexandre F.R.
APPLICANT: LARKIN, Sarah B.
TITLE OF INVENTION: DTEF-1 ISOFORMS AND USES THEREOF
NUMBER OF SEQUENCES: 32
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ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/615,170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Le
8.2e+07;
FILING DATE: 16-JAN-96

ATTORNEY/AGENT INFORMATION:
NAME: Cherskey, Michael J.
REGISTRATION NUMBER: 33,664

REFERENCE/DOCKET NUMBER: ANL-IN-95-027
TELEPHONE: (312) 621-1330
TELEPAX: (312) 621-1330
TELEPAX: (312) 621-0088

INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 5; DB Best Local Similarity 100.0%; Pred. No. 8.2 Matches 5; Conservative 0; Mismatches
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RADESTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 2307U-053120
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 5 bases
TYPE: nucleic acid
STRANDEDNESS: No. 6440671 Applicable
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01526
FILING DATE: 06-FEB 1995
CLASSIFICATION A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/191,493
FILING DATE: 04-FEB-1994
CLASSIFICATION: 435
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INFORMATION FOR SEQ ID NO: 10:
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ATTORNEY/AGENT INFORMATION:
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CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Mizabekov, Andrei D
APPLICANT: Parinov, Sergei V
APPLICANT: Barsky, Victor E
APPLICANT: Kirillov, Eugene V
APPLICANT: Dubiley, Svetlana V
APPLICANT: Dubiley, Svetlana A
TITLE OF INVENTION: Use of Continuous/Contiguous
TITLE OF INVENTION: Use of Continuous/Contiguous
ONRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                               ## SERIERAL INFORMATION:

## APPLICANT: Gilchrest, Barbara A.

## APPLICANT: Gilchrest, Barbara A.

## APPLICANT: Ellex, Mark

## APPLICANT: Ellex, Mark

## APPLICANT: Ellex, Mark

## TITLE OF INVENTION: Use of Locally Applied DNA Fragments

## TITLE OF INVENTION: Use of Locally Applied DNA Fragments

## TITLE OF INVENTION: Use of Locally Applied DNA Fragments

## CURRENT APPLICATION NUMBER: US/09/048,927

## CURRENT FILING DATE: 1998-03-26

## CURRENT FILING DATE: 1996-06-03

## EARLIER PILING DATE: 1996-06-03

## EARLIER PILING DATE: 1995-06-06

## EARLIER FILING DATE: 1995-06-06

## EARLIER FILING DATE: 1995-06-06

## SOFTWARE: Fast SEQ for Windows Version 3.0

## SOFTWARE: Fast SEQ for Windows Version 3.0

## INFORMATION: DNA Fragment

## CONTANT SEATURE:

## OTHER INFORMATION: DNA Fragment

## OTHER INFORM
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ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.50 inch, 1.4 MB storage
CAMPUTER: The Mindows 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: Microsoft Windows 98
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,851
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APPLICATION NUMBER: 08/855,372
FILING DATE: 13-MAY-97
APPLICATION NUMBER: U.S. 08/587,332
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-09-498-851-20/c
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STREET: 20 N. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/09048927
Patent No. 6147056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 CATAC 1
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| Patent No. 6489458
| GENERAL INFORMATION:
| APPLICANT: HACKETT ET AL.
| TITLE OF INVENTION: DNA-BASED TRANSPOSON SYSTEM FOR THE
| TITLE OF INVENTION: INTRODUCTION OF NUCLEIC ACID INTO DNA OF A CELL
| NUMBER OF SEQUENCES: 63
| CORRESPONDENCE ADDRESS: 64
| STREET: 119 NORTH FOURTH STREET, SUITE 203
| CITY: MINNEADLS
| CONTRY: USA
| CONTRY: USA
| CONTRY: USA
| COMPUTER READABLE FORM: 64
| COMPUTER: Floppy disk
| COMPUTER: Floppy disk
| COMPUTER: IBM PC Compatible | COMPUTER: COMPUTER: PLOPS/MS-DOS | COMPUTER: PLOP
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APPLICANT: Gilchrest, Barbara A.
APPLICANT: Gilchrest, Mark
APPLICANT: Biler, Mark
TITLE OF INVENTION: Use of Locally Applied DNA Fragments
FILE REFERENCE: BU94-68A2
CURRENT PELLING DATE: 1998-03-26
CURRENT FILING DATE: 1998-03-26
EARLIER APPLICATION NUMBER: 08/952,697
EARLIER APPLICATION NUMBER: 08/467,012
EARLIER APPLICATION NUMBER: 08/467,012
EARLIER APPLICATION NUMBER: 08/467,012
EARLIER APPLICATION NUMBER: 08/467,012
EARLIER PILLNG DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 7
                                                                                                                                                   LOCATION: 1..7 OTHER INFORMATION: /standard_name= "Rat beta-Myosin OTHER INFORMATION: Heavy Chain M-CAT binding element"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 5; DB 3; Length 7; 100.0%; Pred. No. 5.8e+07;
                                                                                                                                                                                                                                                                                                                                                                                                Length 7;
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                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 5; DB 1; L 100.0%; Pred. No. 5.8e+07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/09048927; Patent No. 6147056; GENERAL INFORMATION:
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                                                                                                       NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
    MOLECULE TYPE: DNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                   US-08-615-170-12
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APPLICANT: AZAKIE, Anthony
APPLICANT: MAR, Janc H.
APPLICANT: MAR, Janc H.
APPLICANT: HALL, Deborah B.
APPLICANT: STEWART, Alexandre F.R.
APPLICANT: STEWART, Alexandre S.2
CORRESPONDENCES: 32
CORRESPONDENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend Khourie and Crew STERET: Stewart Street Tower, One Market Plaza CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 5; DB 1; Length 7; 100.0%; Pred. No. 5.8e+07;
                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
COGATION: 1..7
COTHER INFORMATION: /standard_name= "Sph-II binding
OTHER INFORMATION: site in SV40"
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ZIP: 94105-1493

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/615,170
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01526
FILING DATE: 06-FEB-1995
CLASSIFICATION: 435
CLA
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/191,493
FILING DATE: 04-FEB-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Healin, James M.
REGISTRATION NUMBER: 29,541
REPERENCE/DOCKET NUMBER: 2307U-053120
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12, Application US/08615170
Patent No. 5776776
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100...
5; Conservative
SEQUENCE CHARACTERISTICS:
LENGTH: 7 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                  MOLECULE TYPE: DNA FEATURE:
                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CATAC 5
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us-09-540-843-6.szlm30.rni

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,789A
FILING DATE: May 21, 1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 6523-006
TELEBHONE: (212) 799-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/08646789A
Patent No. 6022863
GENERAL INFORMATION:
APPLICANT: Peyman, John A.
TITLE OF INVENTION: REGULATION OF GENE EXPRESSION
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (212) 869-9741/8864
                                                                                                                                                                                                     MOLECULE TYPE:
DESCRIPTION: Genomic DNA
     APPLICATION NUMBER: 07/8
FILING DATE: 22-MAY-1992
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 9 bases
TYPE: nucleic acid
STRANDEDNESS: singular
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212) 869-974:
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 9 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: New York STATE: New York COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                      1 CATAC 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CATAC 5
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US-08-646-789A-80/c
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US-08-646-789A-8/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Nichonagh, Kevin T.
APPLICANT: McDonagh, Kevin T.
APPLICANT: Nichonagh, Kevin T.
APPLICANT: Nichonagh, Kevin T.
APPLICANT: Nichonagh, Kevin T.
APPLICANT: Tolstoshev, Paul
TITLE OF INVENTION: IMPROVED EXPRESSION OF HUMAN
TITLE OF INVENTION: MULTIDRUG RESISTANCE GENES AND IMPROVED
TITLE OF INVENTION: SELECTION OF CELLS TRANSDUCED WITH SUCH GENES
OWNERSPONDENCES: 19
CORRESPONDENCE ADDRESS: 3
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
STREET: 6 Becker Farm Road
STREET: 6 Becker Farm Road
STREET: 100 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/142,593
FILING DATE: 10-SEP-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/040,664
FILING DATE: 11-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/053,868
FILING DATE: 28-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/065,303
FILING DATE: 13-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/04687
FILING DATE: 11-MAR-1998
ATTORNEY/AGENT INFORMATION:
NAME: SANDBERG, VICTORIA A.
REGISTRATION NUMBER: 41,287
REGISTRATION NUMBER: 41,287
REGISTRATION NUMBER: 41,287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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OPERATING SYSIEM.
SOFTWARE: DAY V2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,276
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-08-583-276-1/C
Sequence 1, Application US/08583276
Sequence 1, Application US/08583276
GENERAL INFORMATION:
APPLICANT: McDonagh, Kevin T.
APPLICANT: Nienhuis, Arthur
APPLICANT: Tolstoshev, Paul
TITLE OF INVENTION: MULTIDRUG RESI.
TITLE OF INVENTION: SELECTION OF C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 05-JAN-1996
CLASSIPFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/332,444
FILING DATE: 31-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 11.
TELECOMMUNICATION INFORMATION: 612-305-1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 11-WAR-1991

ATTORNEY/AGENT INFORMATION
NAME: SANDBERG, VICTORIJ
REGISTRATION NUMBER: 41,
ELECOMMUNICATION INFORMATION
TELEFAX: 612-305-1228
TELEFAX: 612-305-1228
TRIEFAX: 612-305-1228
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomi
GROUPY MATCH
TOPOLOGY: 1000.08
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us-09-540-843-6.szlm30.rni

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REBULL 14
US-09-319-648-68
; Sequence 68, Application US/09319648
; Sequent No. 6451530
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Mary
; TITLE OF INVENTION: Pluorescent Nucleotide Analog Hairpin
; TITLE OF INVENTION: Pormation for Detection of Nucleic Acid Hybridization
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPERENCE/DOCKET NUMBER: 015280-288100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFEAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 68:
                                                                       4.5e+07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 68:
                                         100.0%; Score 5; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
US-08-335-565A-27/c
; Sequence 27, Application US/08335565A
; Patent No. 5527671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Li, Kening
APPLICANT: Rouse, Douglas I.
           Query Match
Best Local Similarity luv...
5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                                                                 7 CATAC 3
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Sequence 1, Application US/09048927

Sequence 1, Application US/09048927

Sequence 1, Application US/09048927

Sequence 1, Application US/09048927

Retent No. 6147056

APPLICANT: Gilchreet, Barbara A. APPLICANT: Gilchreet, Barbara A. APPLICANT: Biller, Mark APPLICANT: Blue, Mana APPLICANT: Blue, Mana APPLICANT: Blue, Mana APPLICANT: Blue, Manager. US/09/048,927

CURRENT APPLICATION NUMBER: US/99/048,927

CURRENT FILING DATE: 1998-03-26

EARLIER FILING DATE: 1998-06-06

EARLIER FILING DATE: 1995-06-06

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 3.0

'TWATH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 5; DB 3; Length 9; 100.0%; Pred. No. 4.5e+07;
                                                                                TITLE OF INVENTION:
NUMBER OF SEQUENCES: 101
CORRESPONDENCE 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: U.S.A.
ZIP: 1036-2711
COMPUTER: TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT ADDRES: MAY 21, 1996
CLASSIFICATION NUMBER: US/08/646,789A
FILING DATE: MAY 21, 1996
CLASSIFICATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6523-006
TELECOMMINICATION INFORMATION:
MARIE MISTOCKET NUMBER: 6523-006
TELECOMMINICATION INFORMATION:
MEDIUM TYPE: TOWN TOWN THE TELECOMMINICATION INFORMATION:
MEDIUM TYPE: MAY 21, 1996
CLASSIFICATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6523-006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
Sequence 80, Application US/08646789A Patent No. 6022863 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: DNA Fragment
US-09-048-927-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 100.0
Best Local Similarity 100.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:

OPERATING SYSTEM:

CURRENT APPLICATION INUMBER:

PILING DATE: MAY 2
CLASSIPICATION 180
ATTORNEY/AGENT INFORM:

MAME: MISTOCK, S.
REGISTRATION NUMBER
REFERENCE/DOCKET NUMBER
REFERENCE/DOCKET NUMBER
REFERENCE/DOCKET NUMBER
CONMUNICATION INF
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TITLE OF INVENTION: SELF-ORGANIZING MOLECULAR PHOTONIC
TITLE OF INVENTION: STRUCTURES BASED ON CHROMOPHORE-AND FLUOROPHORE-
TITLE OF INVENTION: CONTAINING POLYNUCLEOTIDES AND METHODS OF THEIR USE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C.
SOFTWARE: Wordberfect (Version 5.0)
SOFTWARE: Wordberfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/23,233
FILING DATE: May 4, 1994
CLASSIFICATION DATA:
APPLICATION UNBER: 07/790,262
FILING DATE: No. 5565322ember 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: MAIRPHY, DAVIG B.
REFERENCE/DOCKET NUMBER: 207/170
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEC 10 NO: 1:
SEQUENCE CHARACTERISTIES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 5; DB 1; L 100.0%; Pred. No. 8.6e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                        NAME: FILLING, Thomas
NAME: FILLING, Thomas
REGISTRATION NUMBER: 34,163
REFERENE/GOCKET NUMBER: HEL0002P
TELEPOWNINICATION INFORMATION:
TELEPHONE: 619-792-8477
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDENESS: single
TOPOLOGY: Linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08232233
Patent No. 5565322
GENERAL INFORMATION:
APPLICANT: Michael J. Heller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Lyon & Lyon |
611 West Sixth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO
FEATURE:
NAME/KEY: misc_feature
LOCATION: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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TYPE: nucleic acid
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STREET: 611 West Si
CITY: Los Angeles
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CATAC 5
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TITLE OF INVENTION: SELF-CREADIZING MOLECULAR PHOTONIC

TITLE OF INVENTION: SELF-CREATIZING MOLECULAR PHOTONIC

TITLE OF INVEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                         COUNTRY:

USA

ZIP: 53701-2113

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/335,565A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
REPERBENCE/DOCKET NUMBER: 960296.93065
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
German, Thomas L.
VENTION: ASSAY FOR VERTICILLIUM DAHLIAE
EQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/250,951
                                TITLE OF INVENTION: ASSAY FOR VERTICILLIUM INUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles and Brady
STREET: 1 South Pinckney St., PO BOX 2113
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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PRIOR APPLICATION NOMBER: US 07/790,262
FILING DATE: 07-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Conservative
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APPLICATION NUMBER:
PILING DATE:
PILING DATE:
CLASSIFICATION: 435
ATTORNEY/ABENT INFORMA
NAME: Seay, Michola
REGISTRATION NUMBER:
REPERBOCE/DOCKET NUM
TELEPHONE: 608-251-91
TOPOLOGY: 110ar
MOLECULE TYPE: DNA (9
COURTY MATCH
OBEST LOCAL SHILLARY
MATCHES
AMATCHES
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    APPLICANT:
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENBE: NO
FRATURE:
NAME-KEY: misc_feature
J. LOCATION: 10
CHER INFORMATION: /note-"Donor chromphore at the 3' T nucleotide"
US-08-232-233-1
                                                                                                                       0; Gaps
                                                                                                 Query Match 100.0%; Score 5; DB 1; Length 10; Best Local Similarity 100.0%; Pred. No. 8.6e+04; Matches 5; Conservative 0; Mismatches 0; Indels
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Sequence 224,

Sequence 11, Appl Sequence 623, Appl Sequence 2220, Appl Sequence 2256, Appl Sequence 12, Appl Sequence 1, Appl Sequence 1, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 13, Appl Sequence 13, Appl Sequence 131, Appl Sequence 13, Appl Sequence 13, Appl Sequence 22, Appl Sequence 22, Appl Sequence 22, Appl Sequence 23, Appl Sequence 22, Appl

US-10-128-560-224
US-10-11-698-11
US-10-21-698-11
US-09-989-789-623
US-09-989-789-6256
US-09-990-186-2220
US-09-990-186-2220
US-09-990-186-2220
US-09-990-186-2220
US-09-990-186-2256
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US-09-999-994-2256
US-09-989-994-2256
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US-09-989-789-1314
US-09-989-789-1314
US-09-989-789-1314

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December 31, 2003, 17:10:00 ; Search time 58.2911 Seconds (without alignments) 296.896 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
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/prodata/1/pubpna/US09_NEW_PUB.seq2:*
               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                        Gapop 10.0, Gapext 1.0
Minimum DB seq length: 0
Maximum DB seq length: 30
Geost-processing: Minimum Match 0*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                   OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                          IDENTITY NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                            US-09-540-843-6
5
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                                                                                                                                                                                                                  Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                          Run on:
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US-09-962-602-7 US-09-962-602-8 US-09-990-186-622 US-09-990-186-636 US-09-990-186-1338

ALIGNMENTS

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1 CATAC 5

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Sequence 17, App Sequence 6, Appl

US-09-927-886-17 US-09-861-014-6

Sequence 11

Sequence

Sequence 6, Appli Sequence 4, Appli Sequence 6, Appli Sequence 178029, Sequence 178029,

Sequence

Query Match Length

Score

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Sequence 178043, Sequence 3, Appli Sequence 7, Appli Sequence 3, Appli

US-10-122-633-4 US-10-122-633-6 US-10-027-632-178029 US-10-027-632-178043 US-10-027-632-178043 US-10-027-632-178043 US-10-122-630-3 US-10-122-630-3 US-10-122-630-3 US-10-122-630-3

1000.0 1000.0 1000.0 1000.0

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Sequence 178029, Application US/10027632

Sublication Vo. US20030204075A9

Sublication Vo. US20030204075A9

Sublication Vo. US20030204075A9

Sublication Vo. US20030204075A9

Sublication No. US20030204075A9

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: IDOJMOTPHISMS in the Human Genome

TITLE OF INVENTION: 108827.129

CURRENT APPLICATION NUMBER: US 60/128,006

PRIOR FILING DATE: 2000-04-20

PRIOR PELICATION NUMBER: US 60/198,676

PRIOR PELICATION NUMBER: US 60/193,483

PRIOR PELICATION NUMBER: US 60/193,483

PRIOR PELICATION NUMBER: US 60/193,483

PRIOR PELICATION NUMBER: US 60/165,363

PRIOR PELICATION NUMBER: US 60/167,363

PRIOR PELICATION NUMBER: US 60/167,363

PRIOR PELICATION NUMBER: US 60/167,363

PRIOR PELICATION NUMBER: US 60/166,363

PRIOR PELICATION NUMBER: US 60/166,002
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100.0%; Score 5; DB 15; Length 5; 100.0%; Pred. No. 6.7e+08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Glichrest, Barbara A.
APPLICANT: Eller, Mark S.
APPLICANT: Faller, Mink S.
APPLICANT: Yaar, Mina
TITLE OF INVENTION: Method to Inhibit Cell Growth Using
TITLE OF INVENTION: Oligonucleotides
FILE REPERENCE: 0054.1088-019
CURRENT PELING DATE: 2002-04-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                         0; Mismatches
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US-10-122-633-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 09/540,843
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: PCT/US01/10162
PRIOR FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/10122633 Publication No. US20030032611A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                         5; Conservative
   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CATAC 5
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US-10-027-632-178029
                                                                         Matches
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Sequence 4, Application US/10122633
Publication No. US20030032611A1
SENERAL INFORMATION:
APPLICANT: Gilchrest, Barbara A.
APPLICANT: Biler, Mark S.
APPLICANT: Blar, Mina
TITLE OF INVENTION: Method to Inhibit Cell Growth Using
TITLE OF INVENTION: Oligomolectides
FILE REFERENCE: 0054-1088-019
CURRENT APPLICATION NUMBER: US/10/122,633
CURRENT APPLICATION NUMBER: US 09/540,843
PRIOR APLICATION NUMBER: US 09/540,843
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 5;
                                                                                                                                                                                                                    Sequence 6, Application US/10122630
Publication No. US20030032610A1
GENERAL INFORMATION:
APPLICANT: Gilchrest, Barbara A.
APPLICANT: Siler, Mark S.
APPLICANT: Yaar, Mina
TITLE OF INVENTION: Method to Inhibit Cell Growth Using
TITLE OF INVENTION: Oligonucleotides
FILE REFERENCE: 0054.1088-018
CURRENT APPLICATION NUMBER: US/10/122,630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 5; DB 15; I
100.0%; Pred. No. 6.7e+08;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: US 08/467,012
PRIOR PILING DATE: 1995-06-06
PRIOR PILING DATE: 1996-06-03
PRIOR PILING DATE: 1996-06-03
PRIOR APPLICATION NUMBER: US 09/048,927
PRIOR PILING DATE: 1998-03-26
PRIOR PILING DATE: 1998-03-26
PRIOR PILING DATE: 2000-03-31
PRIOR PILING DATE: 2000-03-31
PRIOR PILING DATE: 2000-03-31
PRIOR PILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Synthetic DNA Fragment US-10-122-633-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
OTHER INFORMATION: Synthetic DNA Fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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GENERAL INCURANTION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
ITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 10827.129
CURRENT FILING DATE: 2002-04-30
FRIOR PILING DATE: 2000-07-12
PRIOR PLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR PLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR PLICATION NUMBER: US 60/193,483
PRIOR PLICATION NUMBER: US 60/185,218
PRIOR PLICATION NUMBER: US 60/185,218
PRIOR PLICATION NUMBER: US 60/167,363
PRIOR PLICATION NUMBER: US 60/167,363
PRIOR PLICATION NUMBER: US 60/156,358
PRIOR PLICATION NUMBER: US 60/156,358
PRIOR PLICATION NUMBER: US 60/146,002
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Pred. No. 4.8e+08;
O; Mismatches 0;
         PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FRSESEQ for Windows Version 4.0
SEQ ID NO 178029
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 5; Best Local Similarity 100.0%; Pred. No. Matches 5; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 178043, Application US/10027632 GENERAL INFORMATION:
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APPLICANT: Glichrest, Barbara A.; APPLICANT: Eller, Mark S.
APPLICANT: Yaar, Mina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Conservative
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Best Local Similarity
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US-10-027-632-178029
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US-10-027-632-178043
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Sequence 178043, Application US/10027632

Publication No. US20030204075A9

Publication No. US20030204075A9

TIME OF INVENTION:
APPLICAMT: Wang, David G.
TILLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILLE OF INVENTION: Dolymorphisms in the Human Genome
FILLE OF INVENTION: Dolymorphisms in the Human Genome
FILLE OF INVENTION: DOLYMORER: US/10/027,632

CURRENT APPLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-04-24

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/185,358

PRIOR FILING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-09-08

SEQ ID NOS: 325720

SEQ ID NO 178043

LENGTH: 7
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: 108077,129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
FRIOR FILING DATE: 2000-07-12
FRIOR PELICATION NUMBER: US 60/199,676
FRIOR PELICATION NUMBER: US 60/193,483
FRIOR PILING DATE: 2000-03-29
FRIOR APPLICATION NUMBER: US 60/193,483
FRIOR APPLICATION NUMBER: US 60/193,483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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100.0%; Pred. No. 4.8e+08;
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarit:
Matches 5; Conse
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                        TYPE: DNA
ORGANISM: Human
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ORGANISM: Human
LENGTH: 7
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                                                                                                                                                             APPLICANT: SILCHEEF, MARK S.
APPLICANT: Black, Mark S.
APPLICANT: Yaar, Mark S.
TITLE OF INVENTION: Oligonacleotides
TITLE OF INVENTION: Oligonacleotides
TITLE OF INVENTION: Oligonacleotides
FILE REFERENCE: 0054.1088-019
CURRENT APPLICATION NUMBER: US/10/122,633
CURRENT FILING DATE: 2002-04-12
FRICH APPLICATION NUMBER: US 09/540,843
FRICH APPLICATION NUMBER: PCT/US01/10162
FRICH FILING DATE: 2001-03-31
FRICH FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/10122633 Publication No. US20030032611A1 GENERAL INFORMATION:
                                                                                           Sequence 3, Application US/10122633
Publication No. US20030032611A1
GENERAL INFORMATION:
APPLICANT: Gilchrest, Barbara A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Glichrest, Barbara A. APPLICANT: Eller, Mark S. APPLICANT: Yaar, Mina
                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
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US-10-122-633-3/c
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Method to Inhibit Cell Growth Using
TITLE OF INVENTION: Oligonucleotides
FILE REFERENCE: 0054-1088-018
CURRENT APPLICATION NUMBER: US/10/122,630
CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: US 08/467,012
PRIOR APPLICATION NUMBER: PCT/US96/08386
PRIOR FILING DATE: 1995-06-03
PRIOR FILING DATE: 1996-06-03
PRIOR FILING DATE: 1998-03-05
PRIOR FILING DATE: 1998-03-05
PRIOR FILING DATE: 2000-03-31
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SEQ ID NO ...

CASTORIE: 7

TYPE: DNA

ORGANISM: Artificial Seque...

FRATURE: OTHER INFORMATION: Synthetic DNA Fragu...

CAHER INFORMATION: Synthetic DNA Fragu...

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Query Match

Solvery Match

Best Local Similarity 100.0%; Pred. No. 4.8e+08;

Antrac 5; Conservative 0; Mismatches 0; In

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Best Local Similarity 100.0%; Pred. No. 4.8e+08;
Matches 5; Conservative 0; Mismatches 0;
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US-10-122-630-7
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ORGANISM: Artificial Sequence
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Sequence 11, Application US/09142593
Patent No. US20020016975A1
GENERAL INFORMATION:
TITLE OF INVENTION: DNA-BASED TRANSPOSON SYSTEM FOR THE
TITLE OF INVENTION: INTRODUCTION OF NUCLEIC ACID INTO DNA OF A CELL
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Patent No. US20020103152A1
GENERAL INFORMATION:
APPLICANT: Kay, Mark A.
APPLICANT: Kay, Mark A.
ITILE OF INVENTION: Methods of In Vivo Gene Transfer Using a TITLE OF INVENTION: Sleeping Beauty Transposon System
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 5; DB 9; Length 8; 100.0%; Pred. No. 4.2e+08; ive 0; Mismatches 0; Indels
                                                                                                                                                         CITY: MINNEAPOLIS
STATE: MINNEAPOLIS
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPDY disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: PatentIn Release #1.0, Vergion #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/142,593
FILING DATE: 10-SEP-1998
CLASSIFICATION:
                                                                                                                               E: MUETING, RAASCH & GEBHARDT, P.A. 119 NORTH FOURTH STREET, SUITE 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: SANDBERG, VICTORIA A.
REGISTRATION NUMBER: 41,287
REPERBENCE/DOCKET NUMBER: 110.00450101
TELECOMUNICATION INFORMATION:
TELEPHONE: 612-305-1226
                                                                                                                                                                                                                                                                                                                                                                 PRICE APPLICATION DATA:
APPLICATION NUMBER: 60/040,664
FILING DATE: 11-MAR-1997
PRICE APPLICATION DATA:
APPLICATION NUMBER: 60/053,868
FILING DATE: 28-JUL-1997
PRICE APPLICATION DATA:
APPLICATION NUMBER: 60/065,303
FILING DATE: 13-NOV-1997
PRICE APPLICATION NUMBER: 60/065,303
FILING DATE: 13-NOV-1997
PRICE APPLICATION NUMBER: 90/065,303
FILING DATE: 11-MAR-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Matches 5; Conservative
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STREET: 11
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US-09-927-886-17
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| Sequence 6, Application US/09861014
| Patent No. US20020115216A1
| GENERAL INFORMATION:
| APPLICANT: Steer, Clifford
| APPLICANT: Minehan-Stieers, Cheryle
| APPLICANT: Minehan-Stieers, Composition for Delivery of Compounds to CHIBS
| TITLE OF INVENTION: Composition for Delivery of Compounds to CHRENT PRINGE 110, 01330101
| CURRENT PELING DATE: 2001-05-19
| PRIOR FILING DATE: 2001-05-19
| PRIOR FILING DATE: 2001-05-19
| PRIOR FILING DATE: 2001-04-20
| NUMBER OF SEQ ID NOS: 10
| SOFTWARE: PatentIn version 3.0
| SEQ ID NO 6
| LENGTH: 8
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               CURRENT APPLICATION NUMBER: US/09/927,886
CURRENT FILING DATE: 2001-08-10
PRIOR PILING DATE: 1999-10-28
PRIOR PILING DATE: 1999-110-28
PRIOR PILING DATE: 1999-11-17
PRIOR PILING DATE: 1999-11-17
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Direct repeat sequence
US-09-861-014-6
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Best Local Similarity 100..
FILE REFERENCE: STAN-160CIP
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US-09-861-014-6
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December 31, 2003, 11:36:21; Search time 644.443 Seconds (without alignments) 444.364 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Searched: 2888711 seqs, 20454813386 residuces
Apotal number of hits satisfying chosen parameters:
Animum DB seq length: 0
Aximum DB seq length: 30
Aximum Match 08
Maximum Match 108
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AX573603 Sequence
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AX63603373 Sequence AX018748 Sequence AX34036 Sequence AX3153 Synthetic H AR041154 Sequence AR082814 Sequence AR130710 Sequence AR131705 Sequence AR131705 Sequence AX018750 Sequence AX677250 Sequence AX67788 Sequence AX67788 Sequence Sequence 177317 Sequence 24 177620 Sequence 32 AR002583 Sequence score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. linear DNA Gilchrest, B.A., Yaar, M. and Eller, M. Use of locally applied dna fragments Patent: WO 0174342-A 3 11-OCT-2001; TRUSTEES OF BOSTON UNIVERSITY (US) ALIGNMENTS SUMMARIES AX268755 7 bp Sequence 3 from Patent W00174342. AX268755 GI:16541827 AX626182 AX626780 AX629189 AX631580 AX631755 AX018748 AX343036 BD023279 AR285089 AR285099 AX018746 AX523264 AX573600 AR082813 X573602 AR088823 AX58712. X63805. synthetic construct synthetic construct artificial sequences. B Query Match Length D 100.0 100.0 1000.0 100.0 100.0 100.0 Score DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL RESULT 1 AX268755 LOCUS Result Š

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Nielsen, P.E. and Good, L.
Antibitoic-free bacterial strain selection with antisense molecules
Patent: WO 02079467-A 7 10-OCT-2002;
Koebenhavns Univesitet (DK)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Haplotypes of the pla2glb gene
Patent: WO 0212562-A 20 14-FEB-2002;
Genalssance Pharmaceuticals, Inc. (US)
Location/Qualifiers
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Sequence 20 from Patent WO0212562.
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AX268753
AX268753.1 GI:16541825
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BDO83254 10 bp DNA linear PAT 27-AUG-2002 Human matured/activated dendritic cell expression genes.
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Method for determining skin stress or skin ageing in vitro
Patent: WO 02053773-A 482 11-JUL-2002;
HENKEL KGAA (DE)
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1 (bases 1 to 10)
Matsushima,K., Hashimoto,S. and Suzuki,T.
Matsushima,K., Hashimoto,Yte expressing genes
Patent: JP 2001069993-A 133 21-MR-2001;
DAPAN SCIENCE AND TECHNOLOGY CORP
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5/09, COTK14/47, COTK16/18, GOIN33/50, GOIN33/53/A6IK45/00, PC
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    /organism='Homo sapiens (human)'.

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LPS activated human monocyte expressing genes.
BD007857
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/mol_type="genomic DNA"
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/note="Peptide nucleic acid SP4"
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JP 2001069993-A/133
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JP 2001069993-A/133.
Homo sapiens (human)
Homo sapiens
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                                                                                                                                                                                                 AX573610.1 GI:27551280
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synthetic construct
artificial sequences.
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JOURNAL Patent: WO 02079467-
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8 AGTATGA 2
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 3223 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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1larity 100.0%; Pred. No. 9.9e+05;
Conservative 0; Mismatches 0;
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Sequence 3223 from Patent W002053774.
AX626182
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                                       0; Mismatches
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/db_xref="taxon:9606"
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Petersohn, D., Conradt, M. and Hofmann, K. Method for determining homeostasis of the skin Patent: WO 02053774-A 1200 11-JUL-2002; Henkel Kommanditgesellschaft auf Aktien (DE) Location/Qualifiers
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Sequence 1200 from Patent WO02053774.
1. .11
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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100.0%; Pred. No. 9.9e+05;
tive 0; Mismatches 0; Indels
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Method for determining homeostasis of the skin
Patent: WO 20053774-A 3821 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Sequence 6230 from Patent WO02053774.
AX629189
AX629189.1 GI:28457227
                             11 bp DNi
Sequence 3821 from Patent WO02053774.
AX626780
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7 TITLE
7 JOURNAL
8 EATURES
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Gaps ö 100.0%; Score 7; DB 6; Length 11; 100.0%; Pred. No. 9.9e+05; tive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.
Matches 7; Conservative 10 AGTATGA 4 1 AGTATGA 7 ઠે

BASE COUNT ORIGIN

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Search completed: December 31, 2003, 17:09:47 Job time : 644.443 secs

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APPLICANT: Gilchest, Mina
APPLICANT: Saar, Mina
APPLICANT: Eller, Mark
APPLICANT: Eller, Mark
APPLICANT: Eller, Mark
TITLE OF INVENTION: Use of Locally Applied DNA Fragments
FILE REFERENCE: BU94-68A2
CURRENT APPLICATION NUMBER: US/09/048,927
CURRENT PILING DATE: 1996-03-26
EARLIER APPLICATION NUMBER: 08/457,012
EARLIER PILING DATE: 1996-06-03
EARLIER PILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 4
SCOTTWARE: FASTESEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: ABLESEQ for Windows Version 3.0
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Sequence 1, Application US/09048927

GENERAL INFORMATION:

APPLICANT: Gilchrest, Barbara A.

APPLICANT: Yaar, Mina

APPLICANT: Eller, Mark

TITLE OF INVENTION: Use of Locally Applied DNA Fragments

FILE REFERENCE: B1094-68A2

CURRENT FILING DATE: 1998-03-26

EARLIER APPLICATION NUMBER: 08/952,697

EARLIER APPLICATION NUMBER: 08/952,697

EARLIER APPLICATION NUMBER: 08/467,012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 7; DB 3; Length 7; Best Local Similarity 100.0%; Pred. No. 5.9e+07; Matches 7; Conservative 0; Mismatches 0; Indels
                                             US-08-758-306-367

US-08-758-306-319

US-08-758-306-371

US-08-758-306-815

US-08-758-306-815

US-08-671-320-6

US-08-68-577-6

US-08-985-113-2

US-08-985-162-444

US-08-985-162-444

US-08-985-162-444
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US-08-363-585-55
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US-08-928-692-48
US-08-474-379C-8
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Patent No. 6147056
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                       December 31, 2003, 14:40:05 ; Search time 27.2025 Seconds (without alignments) 113.581 Million cell updates/sec
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.: /cgn2 = /ptodata1/ina/5B COMB.seq:*

.: /cgn2 = /ptodata1/ina/6A COMB.seq:*

.: /cgn2 = /ptodata1/ina/6B COMB.seq:*

.: /cgn2 = /ptodata1/ina/6B COMB.seq:*

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                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-048-927-1

US-09-922-445-12

US-08-922-445-22

US-08-133-27

US-08-134-847-24

US-08-34-847-24

US-08-34-847-327

US-08-34-847-327

US-08-34-847-327

US-08-71-121-4

US-08-71-121-4

US-08-71-131-28

US-08-94-71-44-34

US-09-049-190-6

US-09-049-190-6

US-09-038-073-1315

US-09-038-073-1315
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Searched: 569978 seqs, 220691566 residues

Prinimum DB seq length: 0

Naximum DB seq length: 30

Naximum DB seq length: 30

Naximum Match 08*

Listing first 45 summaries
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-08-256-426B-59
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Maximum Match 100%
Listing first 45 summaries
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Match Length
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Perfect score:
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Gaps

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APPLICANT: Allibert, Patrice A.
APPLICANT: Allibert, Patrice A.
APPLICANT: Mach, Bernard F.
APPLICANT: Mandrand, Bernard F.
APPLICANT: Mandrand, Bernard F.
APPLICANT: Tiercy, Jean-Marie
TITLE OF INVENTION: SYSTEM OF PROBES ENABLING HLA-DR TYPING
TITLE OF INVENTION: TO BE PERFORMED, AND TYPING METHOD USING SAID PROBES
NUMBER OF SEQUENCES:
ADDRESSEE: OLIFF & BERRIDGE
STREET: P.O. Box 10000
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SEQUENCES OF C4-2, A TUMOR SUPPRESSOR GENE,
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,133
FILING DATE: 7-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/030,143
FILING DATE: 11-MAR-1993
CLASSIFICATION: 435
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 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                   Sequence 27, Application US/08485133
Patent No. 5976708
GENERAL INFORMATION:
APPLICANT: Allibert, Patrice A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08744905A
Patent No. 5990294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Murphy, Gerald
APPLICANT: Boynton, Alton
APPLICANT: Sehgal, Anil
TITLE OF INVENTION: NUCLEOT
TITLE OF INVENTION: SEQUENC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 100.
Salara 7; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
7; Conservative
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STATE: Virginia
ZIP: 22320
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US-08-744-905A-4/c
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APPLICANT: Berglund, Lars G. T.
APPLICANT: Berglund, Lars G. T.
APPLICANT: Rendland, Rikard H.
APPLICANT: Rendland, Rikard H.
APPLICANT: Adam, Gail I. R.
TITLE OF INVENTION: REAGENTS AND METHODS FOR DETECTION OF HEART FAILURE
CURRENT APPLICANTION NUMBER: US/09/922,445
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PatentIn version 3.1
SEQ ID NO 22
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Andersson, Maria K.
APPLICANT: Berglund, Lars G. T.
APPLICANT: Berglund, Lars G. T.
APPLICANT: Reneland, Rikard H.
APPLICANT: Adam, Gail I. R.
TITLE OF INVENTION: REAGEN'S AND METHODS FOR DETECTION OF HEART FAILURE FILE REFERENCE: GG126US
CURRENT APPLICATION NUMBER: US/09/922,445
CURRENT FILING DATE: 2010-08-03
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PATENTIN version 3.1
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                                                                                                                                                                                                                                                 0; Mismatches
 EARLIER FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
                                                                                                                                                                                                            100.0%; Score 7; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                Sequence 22, Application US/09922445 Patent No. 6528268
                                                                                                                                ; FEATURE:
; OTHER INFORMATION: DNA Fragment
US-09-048-927-1
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                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 7; Conservative
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Matches 7; Conservative
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Best Local Similarity
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ORGANISM: synthetic
BS-09-922-445-12
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; ORGANISM: synthetic
US-09-922-445-22
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Fatent No. 5693532
GENERAL INFORMATION:
APPLICANT: Parco, Pam
APPLICANT: Draper, Kenneth
APPLICANT: Parco, Pam
APPLICANT: Parco, Pam
APPLICANT: Parco, Pam
APPLICANT: Woolf, Tod
TITLE OF INVENTION: INHIBITING RESPIRATORY
TITLE OF INVENTION: SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 909
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Saite 4700
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS S.O
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/334,847
FILING DATE: NO. 569553cember 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATONIE APPLICATION NUMBER:
ATONIEY/ACBIV INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
FELEPHONE: (213) 955-0440
TELEPHONE: (213) 955-0440
TELEPHONE: (213) 955-0440
TELEPHONE: (213) 955-0440
TELEPHONE: (213) 555-0440
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDLUM TYPE: 3." Diskette, 1.44 Mb
MEDLUM TYPE: 3." Diskette, 1.44 Mb
MEDLUM TYPE: Btorage
COMPUTER: IBM Compatible
OOFBTATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/334,847
FILING DATE: NO. 5693532ember 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 23,327
REGISTRATION NUMBER: 23,327
REFERENCE/DOCKET NUMBER: 209/032
TELECOMMUNICATION INFORMATION:
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Best Local Similarity 71.4
Matches 5, Conservative
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100.0%; Pred. No. 8.6e+03;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PILLON NUMBER: US/08/744,905A
CLASSIFICATION NUMBER: US/08/744,905A
CLASSIFICATION: 536
PRIOR APPLICATION: 536
ATOCNEY/AGENT INFORMATION:
NAME: Baldwin, Geraldine F
REGISTRATION NUMBER: 31,232
REFERENCE/DOCKET NUMBER: 8511-009
TELEPHONE: (212) 869864
TELEPHONE: (212) 869864
CHIERCOMUNICATION INFORMATION:
TELEPHONE: (212) 869864
CHIERCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FRATURE:
COCATION: 1
COCATIO
   TITLE OF INVENTION: AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 24, Application US/08334847
Patent No. 5693532
GENERAL INFORMATION:
APPLICANT: McSwiggen, James
APPLICANT: Draper, Kenneth
APPLICANT: PavCo, Pam
APPLICANT: PavCo, Pam
APPLICANT: Woolf, Tod
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: INHIBITING RESPIRATORY
TITLE OF INVENTION: SYNOYTIAL VIRUS
NUMBER OF SEQUENCES: 909
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                          COUNTE: Na
COUNTE: Na
COUNTE: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: PASTERI DOS
SOFTWARE: PASTERI DOS
SOFTWARE: PASTERI DOS
SOFTWARE: PASTERI DOS
FILING DATE: OS-NOV-1996
CLASSIFICATION NUMBER: US/08/744,905A
FILING DATE: DATE: DATE: DATE: DATE
APPLICATION NUMBER: 31,232
REPERRINGE/DOCKET NUMBER: 31,232
REFERENCE/DOCKET NUMBER: 8511-009
TELEFAX: (212) 8698684
TELEFAX: (212) 8698684
TELEFAX: (212) 8698684
TELEFAX: (212) 8698684
TELEFAX: CALALL PENNIE
CINFORMATION FOR SEQ ID NO: 4:
SEQUIRNCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                 NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O Query Match

Matches 7; Conservative

Matches 7; Conservative

Matches 1 AGTATGA 7

Matches 1 AGTATGA 8

Matches 1 AGTATGA 8
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Sequence 4, Application US/08747121
Patent No. 5874290
GENERAL INFORMATION:
APPLICANT: Murphy, Gerald
APPLICANT: Boynton, Alton
APPLICANT: Schgal, Ani
TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID
TITLE OF INVENTION: SEQUENCES OF A D2-2 GENE ASSOCIATED WITH
TITLE OF INVENTION: BRAIN TUMORS AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,121
FILING DATE: 08-NOV-1996
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION TOWNER:
APPLICATION TOWNER:
APPLICATION TOWNER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
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REGISTRATION NUMBER: 31,232
REFERENCE/DOCKET NUMBER: 8511-008
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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Best Local Similarity
T; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                 Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 15;
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100.0%; Pred. No. 8.6e+03;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 7; DB 1; 1
Best Local Similarity 71.4%; Pred. No. 8.6e+03;
Matches 5; Conservative 2; Mismatches 0
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MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: no
   (213) 489-1600
                             TELEFAX: (213) 955-0440
TELEX: (7-3510
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                          LENGTH: 15 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity
Matches 7; Conserv
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TELEPHONE:
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TOPOLOGY:
US-08-334-847-327
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: McSwiggen, James
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
                                                                                                                                                                                                                                                        ; LOCATION: 1
; COTHER INFORMATION: Where N is any nucleotide
VGS-08-747-121-4
                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-585-684B-130
; Sequence 130, Application US/08585684B
; Patent No. 5877021
; GENERAL INFORMATION:
; APPLICANT: StinchComb, Daniel T.
APPLICANT: Jarvis, Thale
(212)7909090
(212)8698864
                                                                                                                                                                                                                                NAME/KEY: Modified Base
                                         TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                LENGTH: 15 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                      nucleic acid
EDNESS: single
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Conservative

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us-u8-485-133-28

| Sequence 28, Application US/08485133 |
| Patent No. 5976789 |
| GENERAL INFORMATION: |
| APPLICANT: Allibert, Patrice A. APPLICANT: Cros, Philippe |
| APPLICANT: Mach, Bernard F. APPLICANT: Mandrand, Bernard F. APPLICANT: Tiercy, Jean-Marie |
| APPLICANT: Tiercy, Jean-Marie |
| TITLE OF INVENTION: TO BE PERFORMED, AND TYPING METHOD USING SAID PROBES INUMBER OF SEQUENCES: 8 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: OLIFF & BERRIDGE |
| STREET: P.O. BOX 19928 |
| CITY: Alexandria |
| STATE: Virginia |
| STATE: Virginia |
| STATE: Propy disk |
| COMPUTER READABLE FORM: |
| COMPUTER: IBM PC compatible |
| COMPUTER: PIPOPY disk |
| COMPUTER: PATENTING SYSTEM: PC-DOS/MS-DOS |
| COMPUTER: PATENTING SYSTEM: PC-DOS/MS-DOS |
| COMPRESSION |
| COMPUTER: PATENTING PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 7; DB 2; Length 15;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,133
FILING DATE: 1-JUN-1995
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/030,143
FILING DATE: 11-MAR-1993
CLASSIFICATION NUMBER: US/08/030,143
FILING DATE: 11-MAR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REFERENCE/DOCKET NUMBER: WPB 28596A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                  FILING DATE: January 16, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/000, 951
FILING DATE: July 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32, 32
REFERENCE/DOCKET NUMBER: 218/078
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1955-0440
TELEFRAX: (213) 955-0440
                    APPLICATION NUMBER: US/08/585,684B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1315:
SEQUENCE CHARACTERICSICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71.48;
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Matches 5; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
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5 AGUAUGA 11
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Cacaba-1315

Sequence 1315, Application US/085856848

Sequence 1315, Application US/085856848

General No. 5877021

GENERAL INFORMATION:
APPLICANT: Strinchcomb, Daniel T.
APPLICANT: Jarvis, Thale
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
NUMBER OF SEQUENCES: 2751
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 631 Wenet Fifth Street
STREET: 631 Wenet Fifth Street
STREET: 6016 Angeles
CITY: Los Angeles
STATE: California
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tive 2; Mismatches 0; Indels
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COUNTY: U.S.A.

ZIP: 90071

ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 8torage
COMPUTER: 1BM Compatible
OPERATING SYSTEM: 1BM P.C. DOS 5.0
SOFTWARE: 1BM COMPAT: 4PPLICATION NUMBER: US/08/885,684B
FILING DATE: JANUAR: 4000,951
FILING DATE: JANUAR: 4095
ATTORNEY AGENT INFORMATION:
NAME: WATDLEY RICHARD
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELEPONNICATION INFORMATION:
TELEPONICATION INFORMATION INFORMATION:
TELEPONICATION INFORMATION:
TELEPONICATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ VERSION 1.5
CURRENT APPLICATION DATA:
                                                                                               ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
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Best Local Similarity 71.4
Matches 5; Conservative
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EDNESS: single
NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
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ZIP: 90071
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PRIOR APPLICATION TELLING DATE:
ATCHARE: Warbur NAME: War
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Sequence 34, Application US/09094714A

Fatent No. 6117847

GENERAL INFORMATION:
FAPPLICANT: C. Frank Bennett, Nicholas M. Dean
TITLE OF INVENTION: OLIGONUCLEOTIDES FOR ENHANCED MODULATION OF
TITLE OF INVENTION: PROTEIN KINASE C EXPRESSION
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6117847ris, LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                  US-09-094-714A-34/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: P. COUNTRY:
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APPLICANT: C. Frank Bennett, Nicholas M. Dean
APPLICANT: C. Frank Bennett, Nicholas M. Dean
TITLE OF INVENTION: OLIGONUCLEOTIDES FOR ENHANCED MODULATION OF
TITLE OF INVENTION: PROTEIN KINASE C EXPRESSION
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. 6117847ris, LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
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                                                                                                                                 100.0%; Score 7; DB 2; Length 15; 100.0%; Pred. No. 8.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 1910 3A
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/094,714A
FILING DATE: June 15, 1998
CLASSIFICATION NUMBER: 08/601,269
FILING DATE: 14-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/478,178
FILING DATE: 09-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/089,996
FILING DATE: 09-JUL-1993
PROR APPLICATION DATA:
APPLICATION NUMBER: 08/085,852
FILING DATE: 16-MAR-1992
ATTORNEY/AGENT INFORMATION:
ANAMERICATION NUMBER: 17-03324
                                                                                                                                                                                                       0; Mismatches
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US-09-094-714A-33/C

US-09-094-714A-33/C

Sequence 33, Application US/09094714A

Sequence 34, Application US/09094714A

Sequence 37, Application US/09094714A

GENERAL INFORMATION:

APPLICANT: C. Frank Bennett, Nichola APPLICANTION: PROTEIN KINASE CITTLE OF INVENTION: PROTEIN KINASE CITTLE OF INVENTION: PROTEIN KINASE CITTY: Philadelphia STREET: One Liberty Place - 46th F STREET: One Libe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Paul K. Legaard
REGISTRATION NUMBER: 38,534
REFERENCE/DOCKET NUMBER: IS
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INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
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                                                                                                  Query Match
Best Local Similarity luv...
7; Conservative
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Matches 7; Conservative
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                               ; TOPOLOGY: linear
US-08-485-133-28
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STRANDEDNESS:
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    Search completed: January 1, 2004, 00:32:18 Job time : 27.3136 secs
                                                                                                                                                                                                                                                                   NAME: Paul K. Legaard
REGISTRATION NUMBER: 38,534
REFERENCE/DOCKET NUMBER: ISIS-2943
TELECOMMUNICATION:
TELEPHONE: (215) 568-3100
                                                                                                                                                                                                                                                                                                                         TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
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TOPOLOGY: linear
US-09-094-714A-34
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1 AGTATGA 7

AGTATGA

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December 31, 2003, 11:36:21 ; Search time 828.57 Seconds (without alignments) 444.364 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                               nucleic search, using sw model
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                                                                                          Scoring table:
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                          OM nucleic
                                                                                                                                                                            09980559 on 05/19/2004
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                                       Run on:
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KCNO pota Antisence Sequence RabGDI-al Rab GDI a Method fo Sequence Sequence Antisence Sequence Sequence Sequence Sequence Seguence Sequence Seguence Sequence Seguence Sequence score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. AX573597 AX573597 AX573597 AX573597 AX130719 AR130719 AR039512 AR039521 AR039521 AR039521 AR039521 AX693123 AX693124 AX693124 AX693127 AX693127 AX693129 AX693129 AX693129 AX693129 AX693129 AX693130 AX693130 AX693130 AX693131 AX593131 AX70827 AX708 AX708 BD162110 | AR297230 | BD082245 | AX338664 | AX493338 | AX493338 | AX493338 | AX693697 | AX693699 | AX693699 | AX693699 | AX693700 | SAX693700 | SAX693 SUMMARIES AX268753 AX573597 B Length Query Match Score

9 bp Sequence 1 from Patent WO0174342. AX268753 AX268753.1 GI:16541825 synthetic construct synthetic construct artificial sequences.

DEFINITION ACCESSION VERSION KEYWORDS SOURCE

RESULT 1 AX268753 LOCUS

ORGANISM

PAT 29-OCT-2001

linear

DNA

ALIGNMENTS

Sequence Seguence Sequence

Seguence Sequence Sequence

Sequence

Gilchrest, B.A., Yaar, M. and Eller, M. Use of locally applied dna fragments Patent: WO 0174342-A 111-OCT-2001; TRUSTEES OF BOSTON UNIVERSITY (US) REFERENCE AUTHORS TITLE JOURNAL

Pred. No. is the number of results predicted by chance to have a

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Nielsen, P.E. and Good, L.
Antibitotic-free bacterial strain selection with antisense molecules
Patent: WO 02079467-A 10 10-OCT-2002;
Koebenhavns Univesitet (DK)
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                                                                                                                                                                                                                                                                                                                                                                               PAT 07-JAN-2003
/note="The polypeptide KFFKFFFK (SEQ ID NO:1) is linked to N-terminal of the PNA sequence via the ethylene glycol linker called 'eg1'"
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Nielsen, P.B. and Good, L.
Methods of bacterial gene function determination using peptide nucleic acids
Patent: US 6190866-A 6 20-FEB-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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9.1e+04;
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Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 9; Conservative 0; Mismatches 0;
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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ive 0; Mismatches
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Sequence 10 from Patent WO02079467.
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Sequence 6 from patent US 6190866.
AR130719
AR130719.1 GI:14119044
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/organism="unknown"
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Best Local Similarity 100. Matches 9; Conservative
                                                                                                                                                             Similarity 100.
9; Conservative
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ORIGIN
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ACCESSION
VERSION
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AR130719/c
                                                                        BASE COUNT
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VERSION
KEYWORDS
SOURCE
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TITLE
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Antibiotic-free bacterial strain selection with antisense molecules
Patent: WO 02079467-A 7 10-OCT-2002;
Koebenhavns Univesitet (DK)
Location/Qualifiers
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Antibiotic-free bacterial strain selection with antisense molecules
Patent: WO 02079467-A 20 10-0CT-2002;
Koebenhavns Univesitet (DK)
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/organism="synthetic construct"./
/or_type="genomic DNA"
/db_xref="taxon:32630"
/note="Synthetic DNA Fragment"
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100.0%; Pred. No. 4.5e+09;
ative 0; Mismatches 0;
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db xref="taxon:32630"
/note="Peptide nucleic acid SP4"
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/organism="synthetic construct"
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Sequence 7 from Patent WO02079467.
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E 1 (bases 1 to 17)

S Stinchcomb, D.T. and McSwiggen, J.A.

Interleukin-2 receptor gamma-chain ribozymes

NAL Patent: US 5807743-A 371 15-SEP-1998;

Location/Qualifiers

Location/Qualifiers
            1 (bases 1 to 17)
Stinchcomb, D.T. and McSwiggen, J.A.
Interleukin-2 receptor gamma-chain ribozymes
Patent: US 5807743-A 367 15-SEP-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 17)
Stinchcomb, D.T. and McSwiggen, J.A.
Interleukin-2 receptor gamma-chain ribozymes
Patent: US 5807743-A 369 15-SEP-1998;
Location/Qualifiers
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hes 0;
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Seguence 369 from patent US 5807743.
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Sequence 371 from patent US 5807743.
AR039523.1 GI:5958886
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1 (Dases 1 to 15)
Nielsen.P.E. and Good,L.
Nielsen of bacterial gene function determination using peptide nucleic acids
Patent: US 6190866-A 7 20-FEB-2001;
Location/Qualifiers
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Stinchcomb, D.T. and McSwiggen, J.A.
Interleukin-2 receptor gamma-chain ribozymes
Patent: US 5807743-A 365 15-SEP-1998;
Location/Qualifiers
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AR039519
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Sequence 7 from patent US 6190866.
AR130720 AR130720.1 GI:14119045
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Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
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                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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ORGANISM Homo sapiens (human)

REFERENCE
I MATTHORS
Shannon, M., Oul.Y. and Nguyen, C.T.

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(c) 1993 - 2003 Compugen Ltd.
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Searched: 2552756 segs, 1349719017 residues

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Maximum Match 0*

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Listing first 45 summaries
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Melanogenesis asso Peptide nucleic ac Antieense oligonuc Antisense oligonuc Oligonucleotide pr Oligonucleotide pr Oligonucleotide se Description SUMMARIES AAZ10692 AAS14905 AAL44343 ABX15951 ABX15964 ABI05192 ABI06838 ABI06839 ü DB Query Match Length 12201099 1000.00 1000.00 1000.00 1000.00 Score **თთთთთთთ** 45978 Result š υυυ

AAZ10692; 23-NOV-1999 (first entry) Oligonucleotide sequence that increases p53 activity in a cell. Oligonucleotide sequence that increases p53 activity in a cell. UV-induced hyperprobliferative disease; psoriasis, vitligo; atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging; skin cancer; ss. Synthetic. GB2336157-A. 13-OCT-1999; 99GB-0006758. 24-MAR-1999; 98US-0048927. (UVBO-) UNIV BOSTON. Gilchrest BA, Yaar M, Eller M;	ID AAZ10692 standard: DNA: 9 BP.	d: DNA: 9 DF.
23-NOV-1999 (first entry) Oligonucleotide sequence that increases p53 activity in a cel p53 activity, UV mimetic; UV-irradiation; UV-induced dermatos UV-induced hyperproliferative disease; psoriasis; vitiligo; atopic dermatitis; allergic rhinitis; conjunctivitis; photoag skin cancer; ss. Synthetic. 282336157-A. 24-MAR-1999; 99GB-0006758. 26-MAR-1999; 98US-0048927. Gilchrest BA, Yaar M, Eller M;	AAZ10692;	
Obligonucleotide sequence that increases p53 activity in a cell graduation of the control of the	23-NOV-1999 (fir	rst entry)
p53 activity; UV mimetic; UV-irradiation; UV-induced dermatos UV-induced hyperproliferative disease; psoriasis; vitiligo; acopic dermatitis; allergic rhinitis; conjunctivitis; photoag skin cancer; ss.  Synthetic.  28-MAR-1999; 99GB-0006758.  26-MAR-1999; 98US-0048927.  (UYBO-) UNIV BOSTON.  Gilchrest BA, Yaar M, Eller M;	Oligonucleotide s	sequence that increases p53 activity in a cell.
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WPI; 1999-543520/46.	WPI; 1999-543520/46.	/46.

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cell and reducing

activity in

susceptibility to UV-induced hyperproliferative diseases

Claim 11; Page 29; 44pp; English.

DNA fragments useful for increasing p53

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Melanin, melanogenic, oligomer, cytostatic, anti-allergic, p53; anti-inflammatory; dermatological, ophthalmological, anti-psoriatic; immunosuppressive, DNA repair; proliferation inhibitor; apoptosis; tumour necrosis factor inhibitor; photoaging; hyperproliferative disease; carcinoma, oxidative stress; skin cancer; allergy mediated inflammation; conjunctivitis; allergic rhinitis; vitiligo; ss.
                                                                                                                                                       AAZ10692-97 represent DNA fragments that are used for increasing p53 activity in a cell. The oligonucleotides are are UV mimetics and protect cells against subsequent exposure to UV-irradiation or chemicals. The oligonucleotides are useful for increasing p53 activity in a cell, reducing the susceptibility to UV-induced hyperproliferative disasses, treating psoriasis, vitiligo, atopic dermatitis, allergic rhintis, conjunctivitis, and UV-induced dermatoses, reducing photoaging and reducing susceptibility to skin cancer.
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modified base
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PT DNA fragmen

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XX

XX

XX

Claim 11; F

CC AAZ10692-97

CC Cactivity irr

CC chemicals

CC chem
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anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and immunosuppressive activities, function as 'ultra-violet mimics' to induce that processes (or a protective response to later exposure to radiation or chemicals), as a proliferation inhibitor, apoptosis inducer or a tumour necrosis factor inhibitor. Probably they mimic products of the processed UNA-damage intermediates, by inducing the p53 pathway, resulting in transient arrest of cell growth, allowing more time for DNA repair to occur before cell division takes place. The method is especially used to treat cartinoma but may also be used to: treat onther hyperproliferative states (e.g. psoriasis or precancerous conditions); reduce photoaging, oxidative stress or damage; prevent skin cancer; treat allergically mediated inflammation (atopic or contact dermatitis, allergically mediated inflammation); prevent or reduce DNA damage in cells caused by radiation or chemicals; increase melanin production promote apoptosis in epithelial cells (e.g. for treating vitiligo), and to promote apoptosis in epithelial cells (e.g. for treating vitiligo), and to promote apoptosis in response to DNA damage, in epithelial cells (e.g. for treating vitiligo), and to oligonucleotides that contain non-hydrolyzable backbones are used to inhibit apoptosis, in response to DNA damage, in epithelial cells that contain damaged of the oligonucleotides used to inhibit mammalian epithelial cell the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "This sequence is a peptide nucleic acid, (i.e. it contains a polyamide backbone instead of a deoxyribose backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PNA oligomer; PNA; peptide nucleic acid; polyamide backbone; 88; aminoethylglycine; aeg; aminoethylprolyl; aep; aminoethylpyrxolidine; pyr; gene downregulation; bacterial infection; viral infection; cancer; metabolic disease; immunological diseorder; PNA-clamping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gapa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 9; DB 23; L 100.0%; Pred. No. 2.9e+08;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence 9 BP; 3 A; 0 C; 4 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide nucleic acid (PNA) oligomer #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-NOV-2001; 2001WO-DK00779.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-NOV-2000; 2000DK-0001776.
06-MAR-2001; 2001DK-0000371.
16-JUL-2001; 2001DK-0001117.
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/mod_base= (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAL44343 standard; DNA; 10
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Best Local Similarity luv...
9, Conservative
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modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAL44343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAL44343/C
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us-09-540-843-1.szlm30.rng

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The invention relates to selecting genetically modified cells comprising:

(a) modifying cells containing a growth essential gene X, with a vector containing gene Y; and (b) treating the modified cells with an antisense or antigene construct directed against the essential gene X of the cells or antigene construct directed against the essential gene X of the cells to obtain preferential growth of the modified cells over other nonmodified cells. Also included is a product manufactured fully or partially by use of the new method. The method is useful for selecting genetically modified cells and manufacturing a product. It is useful for cresearch the isolation and industrial growth maintenance of transformed organisms. The new method has the advantage of selecting and maintaining a plasmid containing bacterial culture without the use of antibiotics. This has a wide variety of applications in research, development, and industrial production involving genetically modified micro-organisms. The method inhibits bacterial infections in eukaryotic cell cultures.

The present sequence is an antisense oligonucleotide (incorporated into a peptide nucleic acid (PPAA) melecule) which targets the E. coli acpp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "C is covalently linked to the peptide appearing as ABG73942 via a polyethylene glycol moiety"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AcpP; antisense; ss; protein nucleic acid; PNA; bacterial infection; genetically modified micro-organism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /bound moiety= "Bases 15..6 of the acpP sequence
appearing as ABX15967"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /bound moiety= "Bases 15..6 of the acpP sequence appearing as ABX15966"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 9; DB 25; I 100.0%; Pred. No. 1.1e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10 BP; 2 A; 4 C; 0 G; 4 T; 0 other;
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/note= "T is amidated"
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                 Claim 24; Page 52; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   base= OTHER
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Best Local Similarity 100.
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/*tag=
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/mod_ba
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modified_base
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                 셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                    The invention comprises peptide nucleic acid (PNA) oligomers, where the single units of the oligomers comprise different amino acid backbones belected from any amino acid, such as: including aminochylylyine (aeg); aminochylpyrrolidine (pyr). The PNA oligomers of the invention are useful for the downregulation of specific genes by targeting the genes at the mRNA or DNA level. The PNA oligomers are useful for treating bacterial and viral infections, cancer, metabolic diseases and immunological disorders. The PNA oligomers are also useful in PCR monitoring/modulation by PNA-clamping. The present DNA sequence represents a PNA oligomer of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Selecting genetically modified cells useful for isolation and industrial growth of transformed organisms comprises treating the modified cells with an antisense or antigene construct directed against the essential gene X of the cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AcpP; antisense; ss; protein nucleic acid; PNA; bacterial infection; genetically modified micro-organism.
                                                                                                                           New peptide nucleic acid oligomer, useful as antisense molecules to treat bacterial and viral infections, has single units comprising different amino acid backbones such as aminoethylglycine -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
/mod_base= OTHER
/note= "C is covalently linked to a Lysine residue"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 9; DB 24; Length 10; 100.0%; Pred. No. 1.1e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10 BP; 2 A; 4 C; 0 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                               Example 7; Page 34; 40pp; English.
MAPI; 2002-490198/52.

MAPI; 2002-490198/52.

New peptide nucleic acid oligome:
    treat bacterial and viral infect:
    Treat invention comprises peptide is ingle units of the oligomers of commonethylprolyl (acp); and aminoethylprolyl (acp); and immunological disorcent in PCR monitoring/modulation by increases and immunological disorcent in PCR monitoring/modulation by increases and immunological disorcent increases and increa
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Gaps

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.

ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
                                                                                                                                              This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.

ABCCOOLO-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIFO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide primer SEQ ID NO 306811 for detecting SNP TSC0022179.
                designed to detect single nucleotide polymorphisms and cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID 306811; 29pp + Sequence Listing; German.
                                                                                            Claim 1; SEQ ID 305165; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Set of oligonucleotides, useful for diagnosis and cell designed to detect single nucleotide polymorphisms and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 9; DB 23; I
100.0%; Pred. No. 1.1e+04;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12 BP; 5 A; 0 C; 4 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Berlin K;
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9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EPIG-) EPIGENOMICS AG
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                                            methylation status
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Best Local S
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                ##X & X O O O O O O O O O O O O X & O
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                                                                                                                                                                                                                                                                                                                                                              The invention relates to selecting genetically modified cells comprising:

(a) modifying cells containing a growth essential gene X, with a vector containing gene Y; and (b) treating the modified cells with an antisense or antigene construct directed against the essential gene X of the cells not obtain preferential growth of the modified cells over other nonpartially by use of the new method. The method is useful for selecting genetically modified cells and manufacturing a product. It is useful for research the isolation and industrial growth maintenance of transformed organisms. The new method has the advantage of selecting and maintaining a plasmid containing bacterial culture without the use of antibiotics. This has a wide variety of applications in research development, and industrial production involving genetically modified micro-organisms. The method inhibits bacterial infections in eukaryotic cell cultures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is an antisense oligonuclectide (incorporated into a peptide nucleic acid (PNA) molecule) which targets the E. coli acpP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                             Selecting genetically modified cells useful for isolation and industrial growth of transformed organisms comprises treating the modified cells with an antisense or antigene construct directed against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide primer SEQ ID NO 305165 for detecting SNP TSC0021329.
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                                                                                                                                                                                                                                                                 the essential gene X of the cells
                                                                                                                                                                                                                                                                                                                 Claim 29; Fig 1; 92pp; English.
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DR WPI; 2003-103273/09.

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Selecting genetically modification of trans industrial growth of trans modified cells with an ant PT the essential growth of trans modified cells with an ant PT the essential grow XX

Claim 29; Fig 1; 92pp; Eng XX

Claim 29; Fig 1; 92pp; Eng XX

Containing gene Y; and (b) or antigene construct direct containing gene Y; and (containing gene Y; and (b) or antigene construct direct to obtain preferential grow modified cells organisms. The new method in genetically modified cells organisms. The new method in genetically modified cells organisms. The new method in genetical production involuence in the present sequence is an epetide nucleic acid (PNA) gene (gene X in this exampled onerty Match

Sequence 10 BP; Z A; 4 C; 0

Ouery Match

Matches 9; Conservative Constantive Construction (PNA)

Constantial production (PNA)

Conservative Constantial (PNA)
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WO200177384-A2. Homo sapiens

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Length 12; 0; Indels 3 GAGTATGAG 11

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ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide primer SEQ ID NO 306812 for detecting SNP TSC0022179.
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                                                                                                                                                                           100.0%; Score 9; DB 23; Length 12; 100.0%; Pred. No. 1.1e+04; Ative 0; Mismatches 0; Indels
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                                                                                                                          Sequence 12 BP; 3 A; 0 C; 4 G; 5 T; 0 other;
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                                                                              ftp.wipo.int/pub/published_pct_sequences.
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Best Local Similarity
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic (SNP) oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABIS2073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                             Oligonucleotide primer SEQ ID NO 321106 for detecting SNP TSC0030074.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Best Local Similarity 100.00
Best Local 9; Conservative
ABI21133 standard; DNA; 12
                                                                                                                     (first entry)
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC10010-ABIS2973 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide nucleic acid; PNA; bacterial infection; 23S ribosomal RNA; rRNA;
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/mod_base= OTHER
/mote= "OTHER = T monomer comprising
/note= "OTHER = T monomer comprising
N-(2-Boc-aminoethyl)-N-(thymine-1-yl-acetyl)
derived from an unknown amino acid"
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/mod_base= OTHER
/note= "OTHER = T monomer comprising
/note= "OTHER = T monomer comprising
N-(2-Boc-aminoethyl)-N-(thymine-1-yl-acetyl)
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N-(2-Boc-aminoethyl)-N-(thymine-1-yl-acetyl)
derived from an unknown amino acid"
                                                                                                                           Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine methylation status -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 9; DB 23; Length 12; Best Local Similarity 100.0%; Pred. No. 1.1e+04; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                      Claim 1; SEQ ID 347990; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified peptide nucleic acid (PNA) molecule #8.
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                                                     Berlin K;
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                                                     Piepenbrock C,
                 (EPIG-) EPIGENOMICS AG.
                                                                                        WPI; 2001-657177/75
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Gaps

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Length 12;

100.0%; Score 9; DB 23; Length 12; 100.0%; Pred. No. 1.1e+04;

Local Similarity 100.

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1 GAGTATGAG

Sequence 12 BP; 3 A; 0 C; 6 G; 3 T; 0 other;

Oligonucleotide primer SEQ ID NO 347990 for detecting SNP TSC0045390.

07-APR-2000; 2000DE-1019173.

06-APR-2001; 2001WO-IB00713

WO200177384-A2

18-OCT-2001

Homo sapiens

ABI48017 standard; DNA; 12 BP

22-FEB-2002 (first entry)

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABI082073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fip.wipo.int/pub/published_pct_sequences.
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                             WO200177384-A2
                                                                                                                                                                                        Homo sapiens
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\$\$\$X8X\$X8X#X#X#X**@\$\$\$&@#\$%#X%%@\$\$** 

New peptide nucleic acid monomer useful e.g. in the treatment of

Example 1; Page 23; 58pp; English.

immunological disorders

Puschl A;

Nielsen PE, Manoharan M,

WPI; 2002-575409/61

(PANT-) PANTHECO AS

33-JAN-2002; 2002WO-DK00005.

WO200253574-A2

11-JUL-2002

05-JAN-2001; 2001DK-0000021

us-09-540-843-1.szlm30.rng

Unidentified

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used to combat diseases, especially bacterial infections, by targeting molecules such as 23S ribosomal RNA and inhibiting translation. They are molecules such as 23S ribosomal RNA and inhibiting translation. They are useful in the manufacture of a medicament for the treatment of a diseases e.g. bacterial and viral infections, cardiac or vascular diseases.

E. g. bacterial and viral infections cardiac or vascular diseases.

E. g. bacterial and viral infections or inborn errors of metabolism) and immunological disorders. The microorganisms that can be inhibited include Gram-positive organisms (e.g. Streptococcus, Staphylococcus, Peptococcus, Bacillus, Listeria, Clostridium, Propionebacteria, Gram-negative calmonalla, Shigella, Proteus, Pseudomonas, Vibrio, Legionella, Branhamella and organisms which stain poorly with Gram's stain (e.g. Mycobacteria, and organisms which stain poorly with Gram's stain (e.g. Mycobacteria, Coxiella). The PNA molecule enables specific and efficient inhibition of bacterial genes with nanomolar concentrations and enhances antiinfective effect with different orientation of the modified PNA molecule, #8.
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                                /*tag= e
/mod_base= OTHER
/note= "OTHER = T monomer comprising
N-(2-Boc-aminoethyl)-N-(thymine-1-yl-acetyl)lysine
and is a C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention discloses peptide nucleic acid (FNA) monomers which can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide nucleic acid; PNA; bacterial infection; 23S ribosomal RNA; rRNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified peptide nucleic acid (PNA) molecule #8 complementary DNA
                                                                                                                                                                                                                                                                                                                                                                                                           peptide nucleic acid monomer useful e.g. in the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation, viral infection, cardiac disease, vascular disease, metabolic disease, diabetes; metabolism, immunological disorder, Gram-positive, Gram-negative, antiinfective, ss.
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 derived from an unknown amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12 BP; 3 A; 4 C; 0 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                      Puschl A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 23; 58pp; English.
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                                                                                                                                                                                                                        03-JAN-2002; 2002WO-DK00005.
                                                                                                                                                                                                                                                             05-JAN-2001; 2001DK-0000021
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                                                                                                                                                                                                                                                                                                                                    Nielsen PE, Manoharan M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              immunological disorders
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                 WO200253574-A2.
                   modified base
                                                                                                                                                                                      11-JUL-2002.
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The invention discloses peptide nucleic acid (PNA) monomers which can be used to combat diseases, especially bacterial infections, by targeting used to combat diseases, especially bacterial infections, by targeting colecules such as 23% ribosomal RNA and inhibiting translation. They are useful in the manufacture of a medicament for the treatment of a diseases e.g. bacterial and viral infections, cardiac or vascular diseases.

C. G. Bacterial and viral infections, cardiac or vascular diseases.

C. Gram-positive organisms (e.g. diabetes or inhorn errors of metabolism) and immunological disorders. The microorganisms that can be inhibited include Gram-positive organisms (e.g. Streptococcus, Staphylococcus, Peptococcus, Bacillus, insterial, Clostridum, Propionebacterial, Gram-negative bacterial, Glostridum, Propionebacterial, Gram-negative Calmonella, Shigella, Proteus, Pseudomonas, Vibrio, Legionella, Salmonella, Bortella, Campylobacter, Neisseria, Branhamella) and organisms which stain poorly with Gram's stain (e.g. Mycobacteria, The PNA molecule enables specific and efficient inhibition of bacterial genes with nanomolar concentrations and enhances antiinfective effect with different orientation of the peptide in relation to the Nanomolar and officed plan molecule, #8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence 12 BP; 5 A; 0 C; 4 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ABK91038) complementary DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABK91040 standard; RNA; 12 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-JAN-2002; 2002WO-DK00005.
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ABK91040
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05-JAN-2001; 2001DK-0000021.

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used to combat diseases, especially bacterial infections, by trageting molecules such as 23S ribosomal RNA and inhibiting translation. They are useful in the manufacture of a medicament for the treatment of a diseases e.g. bacterial and viral infections, cardiac or vascular diseases, e.g. bacterial and viral infections, cardiac or vascular diseases (e.g. diabetes or inborn errors of metabolism) and immunological disoaces. The microorganisms that can be inhibited include Gram-positive organisms (e.g. Streptococcus, Staphylococcus, Peptococcus, Bacillus, Listeria, Clostridium, Propionebacteria), Gram-negative bacteria (e.g. Bacteroides, Probacterium, Sacherichia, Klabsiella, Bacillus, Brocella, Ruccella, Campylobacter, Neisseria, Branhamella) and organisms which stain poorly with Gram's stain (e.g. Mycobacteria, Treponema, Leptospira, Borrela, Mycoplasma, Clamydia, Rickettsia, Treponema, Leptospira, Borrela, Mycoplasma, Clamydia, Rickettsia, Coxiella). The PNA molecule enables specific and efficient inhibition of bacterial genes with nanowolar concentrations and enhances antinfective effect with different orientation of the peptide in relation to the NAM, sequence. The sequence of the persented is the modified PNA molecule, #8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "This sequence is a peptide nucleic acid, (i.e. it contains a polyamide backbone instead of a deoxyribose backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= b
/mod_base= OTHER
/note= "Optional (3S, 5R) pyrrolidone PNA monomer or (2R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention discloses peptide nucleic acid (PNA) monomers which can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PNA oligomer; PNA; peptide nucleic acid; polyamide backbone; ss; aminoethylglycine; aeg; aminoethylplotlyl; aep; aminoethylpytzolidine; pwr; gene downregulation; bacterial infection; viral infection; cancer; metabolic disease; immunological disorder; PNA-clamping.
                                                                                                                                                                                                                                                                                                                         New peptide nucleic acid monomer useful e.g. in the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 9; DB 24; Length 12; 77.8%; Pred. No. 1.1e+04; tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12 BP; 5 A; 0 C; 4 G; 3 U; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ABK91038) complementary RNA sequence.
                                                                                                                                                                                   Puschl A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 23; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAL44340 standard; DNA; 12 BP.
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                                                                                                                                                                                Nielsen PE, Manoharan M,
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Matches 7; Conservative
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2 GAGUAUGAG 10
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modified_base
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AAL44340;
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The invention comprises peptide nucleic acid (PNA) oligomers, where the single units of the oligomers comprise different amino acid backbones selected from any amino acid, such as: including aminoethylglycine (aeg); and aminoethylpyrzolidine (pyr). The PNA oligomers of the invention are useful for the downregulation of specific genes by targeting the genes at the mRNA or DNA level. The PNA oligomers are useful for treating bacterial and viral infections, cancer, metabolic diseases and immunological disorders. The PNA oligomers are also useful in PCR monitoring/modulation by PNA-clamping. The present DNA sequence represents a PNA oligomer of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                              New peptide nucleic acid oligomer, useful as antisense molecules to treat bacterial and viral infections, has single units comprising different amino acid backbones such as aminoethylglycine -
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                                      /*tag= c
/mod_base= OTHER
/note= "The base is modified with Lys-NH2"
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4S) pyrrolidone PNA monomer (A12)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Page 19; 40pp; English.
                                                                                                                                                                                                                  24-NOV-2000; 2000DK-0001776.
06-MAR-2001; 2001DK-0000371.
16-JUL-2001; 2001DK-0001117.
                                                                                                                                                                                 23-NOV-2001; 2001WO-DK00779.
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Best Local Similarity 100...
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                                                                                                                                                                                                                                                                                                                            Nielsen PE, Pueschl A;
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                                                                                                            WO200242316-A2
                     modified base
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D45824 HUMGS03044 AL766985 Arabidops BG926068 HNC23-1-E

AZ478673 1M0298J20

us-09-540-843-1.szlm30.rst

Run

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AZ658158 22 bp DNA linear GSS 14-DEC-2000 1M0534H17R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0534H17 R, genomic survey sequence.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Malmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
Tel: 80115, 85566
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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BH811671
TAL19504Q
AZ484572
AZ500131
AZ830077
AZ370614
AZ772496
AZ847502
BH86527
AZ810630
AZ811053
BH856297
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Mus musculus
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DEFINITION
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
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             version 5.1.6
- 2003 Compugen Ltd.
                                                                                                                                                                                                                Gapop 10.0, vapear ...

Searched: 22781392 segs, 12152238056 residues

Animum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0*

Maximum Match 100*

Listing first 45 summaries
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                                                                                            December 31, 2003, 13:58:09
                                                               - nucleic search, using sw model
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             GenCore
Copyright (c) 1993
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AZ658158 1M0534H17 BH904074 SALK 1039 BH856420 SALK 0797 AW059679 AHUTH-bss

AZ658158 BH904074 BH856420 AW059679

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Query Match 1

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Result

A1747751 u121h65.x A2358656 1M0101K12 A2357990 1M0261E11 A2391531 2M0275K15 A2606440 2M0668805 A2606440 2M0668805 A2606440 2M068805 A1630912 tz31g03.x A539103 1M0401K07 BH811671 SALK 0595 A1463250 T. bTucei A2484572 1M031B100 A2830077 2M0109006 A2370614 1M0121010 A2830077 2M0109006 A2370614 1M0538H03 A2847502 2M0418C08 BH865517 SALK 0987 A871952 VG43B09.r B0594927 VG43B09.r B0594927 VG43B09.r A2831709 2M0111006 BH865517 SALK 0987 A2831709 2M0111006 BH865517 SALK 0987 A2831709 2M0111006 BH865637 SALK 0810 BH865637 SALK 0810 BH865637 SALK 0810 BH865638 SALK 0840 BH867761 SALK 0840 BES9438 SALK 0840 BZ59438 SALK 0840

Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0534 row: H column: 17 Seg primer: CACACAGGAAACAGCTATGACC Class: plasmid ends

/organism="Mus musculus" /mol\_type="genomic DNA" /strain="C57BL/6J" /db\_xref="taxon:10090" /clone="UUGCIMO534H17"

High quality sequence stop: 22. Location/Qualifiers

source

FEATURES

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                                                                                                                          was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwDA2 (gil 4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xiii0-Gold (Stratagene) cells and selected for ampicillin resistance."
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1 (Dases 1 to 28)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C.J., Oske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
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lines
                                                                                                              (http://www.jax.org/resources/documents/dnares/). The DNA
/lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
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/note="Vector: PWD42nv; Purified genomic DNA from M.
muscul" Collab./60 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
The Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 22;
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceee, Arabidopsis.
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                                                                                                                                                                                                                         /db_xref="taxon:3702"
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/clone="SALK 103904.28.95.x"
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/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements The resultiant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
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A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
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/clone=lb="Ārabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
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                     This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At4g23060. Class: TDNA tagged. Location/Qualifiers
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Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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Email: ecker@salk.edu
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9, Conservative
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BASE COUNT ORIGIN

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (stratagene) cells and selected for ampicillin resistance."
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                                                                               Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 24)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
Mouse whole genome scaffolding with paired end reads from 10kb
Dlasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone lib="Mouse 10kb plasmid UUGCIM library"
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musculus C57NB/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="Male"
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100.0%; Pred. No. 1.8e+05;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ddunnogenetics.utah.edu
Insert Length: 10000 Std Brror: 0
Insert Length: 10000 Std Brror: 20
Seq primer: CACACAGGAAACAGCTATGACC
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/clone="UUGC1M0298J20"
                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Rese
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Location/Qualifiers
                                                              Mus musculus (house mouse)
        AZ478673.1 GI:10637794
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Fax: 801 585 7177
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1 (bases 1 to 24)
Exember, S., Williams, S.R., Vermass, E.H., Storck, T., Moon, K., McCollum, C., Mao, J.I., Kirchner, J.J., Eletr, S., DuBridge, R.B., Burcham, T. and Albrecht, G.
In vitro cloning of complex mixtures of DNA on microbeads: Physical separation of differentially expressed cDNAs
Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 bp mRNA linear EST 23-AUG-2000
AHUTH.best.dhc15.aa.A050g08 DNC15 Homo sapiens cDNA, mRNA sequence.
AW059679
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directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html" 10 10 4 4 9 9 t
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Sequence obtained from LYNX Therapeutics Megasort technology.
Collected from the down-regulated gate.
High quality sequence stop: 24.
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25861 Industrial Blvd., Hayward, CA 94545, USA
Tel: 510 670 9338
sex: 510 670 9302
                                                                                                                                                                  100.0%; Score 9; DB 28; I 100.0%; Pred. No. 4.4e+04;
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100.0%; Pred. No. 1.8e+05;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Burcham TS
                                                                                                                                                                                            Best Local Similarity 100.
Matches 9; Conservative
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us-09-540-843-1.szlm30.rst

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS JOURNAL

TITLE

ACCESSION

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Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence is recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by clone F9L1. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana
Mkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceáe; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B. A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics
                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Saedler, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer
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Arabidopsis thaliana T-DNA flanking sequence GK-215C11-014144,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Itoh, K., Okubo, K., Yosii, J., Yokouchi, H. and Matsubara, K.
An expression profile of active genes in human lung
DNA Res. 1, 279-287 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A pipeline for automated high-throughput generation of RE
(flanking sequence tags) from Arabidopsis thaliana T-DNA
transformed lines
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Li,Y., Rosso,M., Strizhov,N. and Weisshaar,B.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                 Institute for Molecular and Cellular Biology
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Pred. No. 1.9e+05;
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Tel: 06-877-5111 x3910
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100.0%; Pred. No. ...
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AL766985
AL766985.1 GI:21520104
                                                                                                                                                                                                                                                                                                                                                        Contact: Kohichi Itoh
                                                                                                      Homo sapiens (human)
                                                     D45824.1 GI:662778
3', mRNA sequence.
D45824
                                                                                                                                                                                                          1 to 27)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 06-877-1922.
                                                                                                                                                                                                                                                                                                                                                                                                         Osaka University
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                                                                                                                                Homo sapiens
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hes 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gij4732114 [gb]AR123072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (Dases 1 to 25)
Dunn, D., Aoyagi, Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 309, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UTGCIM library"
/note="Vector: PWP4Zlv; Purified genomic DNA from M.
musculus C57BL/6J (Male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                       Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.
Plate: 0427 row: J column: 22
Seq primer: CGTTCTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers
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/organism="Mus musculus"
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="UUGC1M0427J22"
                                                                             musculus (house mouse)
                            AZ605844.1 GI:11728034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                         Mus musculus
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RESULT 7 D45824/c LOCUS DEFINITION

BASE COUNT

ORIGIN

Matches

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Gaps

us-09-540-843-1.szlm30.rst

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/Clone_lib="Sugano mouse embryo mewa"
//clone_loctor: pME18B-FL3; site_l: DraIII (CACTGTGTG);
//ince="Vector: pME18B-FL3; site_l: DraIII (CACTGTGTG);
//ince="Vector: pME18B-FL3; site_l: DraIII (CACTGTGTG);
//with_an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTT];
//double-granded cDNA was ligated to a DraIII adaptor
//double-granded cDNA was ligated to a DraIII adaptor
gites of the pME18S-FL3 vector (5' site CACTGTGTG; 3' site
//ACCATGTG]. XhoI should be used to isolate the cDNA
insert. Size selection was performed to exclude fragments
// Skb. Library constructed by Dr. Sumio Sugano
                                                                                                                                                                                                                                                                                                                                                                                                                                     EST 22-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases I to 19)
Marra M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, F., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
The Washunki Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mouseeer@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ul21h05.xl Sugano mouse embryo mewa Mus musculus cDNA clone
IMAGE:208249 3' similar to TR:P79101 P79101 CLEAVAGE AND
POLYADENYLATION SPECIFITY FACTOR PROTEIN. ;, mRNA sequence.
AI747751. GI:5126015
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Custom primers for sequencing: 5' end primer
CTTCTGCTGTAAAAGTTGCG and 3' end primer
CGACCTGCAGTTCGAGCAAA."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: custom primer used
High quality sequence stop: 1.
Location/Qualifiers
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                                                                                                                                        Indels
                                                                    Score 7.4; DB 12;
Pred. No. 3.8e+05;
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/clone="IMAGE:2088249"
/dev_stage="embryo, 14 dpc"
/lab_host="DH10B"
                                                                                                                                    0; Mismatches
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/organism="Mus musculus"
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/strain="C57BL"
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88.9%;
                                  Query Match
Best Local Similarity 88.9%;
Best Local Similarity 88.9%;
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                                                                                                                                                     /organism="Arabidopsis thaliana"
/mol type="genomic DNA"
/mol type="genomic DNA"
/mol type="genomic DNA"
/mol type="genomic DNA"
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/db_xref="taxon:3702"
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/clone="ibx-abidopsis thaliana T-DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PACISI. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thalaina nuclear genome sequence were processed for submission. T-DNA derived sequences were
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HNC23-1-E10.R HNC (Human Normal Cartilage) Homo sapiens CDNA, mRNA
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Sathe, G., Mui, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA Tel: 610-270-7245
Fax: 610-270-5598
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 17)

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Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-veoln.mpg.de/GABI-Kat/. Location/Qualifiers
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/tishot="E.coli DH10 B"
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/note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88.9%; Score 8; DB 29; Length 30; 100.0%; Pred. No. 2e+05; ive 0; Mismatches 0; Indels
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Seq primer: T7.
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UW2109
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Gaps

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RESULT 11

ACCESSION VERSION KEYWORDS

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of publy (gilfallalghAll29072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to edemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                          AZ457990 19 bp DNA linear GSS 04-OCT-2000 1M0261E11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0261E11 R, genomic survey sequence.

AZ457990.1 GI:10616115
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University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mummalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Walse, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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/note="Wector: PWD42Inv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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/lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
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Length: 10000 Std Error: 0.00
Pred. No. 4e+05;
                           0; Mismatches
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/strain="C57BL/6J"
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/clone="UUGC1M0261E11"
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Fax: 801 585 7177
Email: ddunn@genet
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1 (bases 1 to 18)
2 (bunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Bunn, H., Longacre, S., Mahmoud, M., Menen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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1M0101K12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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/clone lib="Mouse 10kb plasmid UGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G79BL/6J (male) was obtained from the Jackson
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Insert Length: 10000 Std Error: 0.00
Plate: 0101 row: K column: 12
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
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/organism="Mus musculus"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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/clone="UUGC1M0101K12"
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Fax: 801 585 7177
8; Conservative
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source

82.2%; Score 7.4; DB 28; Length 19;

BASE COUNT ORIGIN

us-09-540-843-1.szlm30.rst

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Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                  AZ991531 19 bp DNA linear GSS 27-APR-2001
2M0275K15R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0275K15 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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      82.2%; Score 7.4; DB 28; Length 19; 88.9%; Pred. No. 4e+05; live 0; Mismatches 1; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0275 row: K column: 15
Seq primer: CACACAGGAAACAGCTATGACC
Class: plaemid ends
High quality sequence stop: 19.
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AZ991531.1 GI:13862758
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                                                                           Conservative
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Fax: 801 585 7177
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Query Match
Best Local Similarity
Matches 8; Conserv
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05/19/2004
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pWAP2 (gil 4732114 |gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                               AZ646291 20 bp DNA linear GSS 14-DEC-200 IMO512D07F Mouse 10kb plasmid UUGCIM library Mus musculus genomic Clone UUGCIM0512D07 F, genomic survey sequence.
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                                                                  Gaps
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Score 7.4; DB 28; Length 19;
Pred. No. 4e+05;
                                                              Indels
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Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. 20
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/strain="C578L/6J"
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                                                              0; Mismatches
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University of Utah Genome Center
University of Utah
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/clone="UUGC1M0512D07"
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Score 7.4; DB 28;
Pred. No. 4.2e+05;
0; Mismatches 1;
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                                                                                                    82.2%;
88.9%;
                                                                                                 Query Match
Best Local Similarity 88.9
Matches 8; Conservative
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BASE COUNT
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University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                      AZ806440 21 bp DNA linear GSS 20-FEB-2001 2M0068B05R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0068B05 R, genomic survey sequence.
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1 (bases 1 to 21)
2 (bases 1 to 21)
3 (bases 1 to 21)
4 (bases 1 to 21)
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/clone lib="Mouse 10kb plasmid UGCIM library."
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musculus G57BL/6J (male) was obtained from the Jackson
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                                                                 82.2%; Score 7.4; DB 28; Length 20; 88.9%; Pred. No. 4.1e+05; ive 0; Mismatches 1; Indels
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Insert Length: 10000 Std Error: 0.00
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Class: plaemid ends
High quality sequence stop: 21.
Location/Qualifiers
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/strain="C57BL/6J"
/db xref="taxon:10090"
/clone="UUGC2M0068B05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
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                                  Query Match
Best Local Similarity 88.5
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Fax: 801 585 7177
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DEFINITION
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Sequence Sequence Sequence

Sequence

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OTHER INFORMATION: DNA Fragment
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ORGANISM: Artificial Sequence
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  RESULT 2
US-09-049-190-6/c
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Sequence 6, Appli
Sequence 7, Appli
Sequence 6, Appli
Sequence 7, Appli
Sequence 365, App
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8965, Ap
5455029
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                                                                                                                                                December 31, 2003, 14:40:05 ; Search time 34.9747 Seconds (without alignments) 113.581 Million cell updates/sec
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Sequence 8965,
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                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Gapop 10.0, vaper...

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S69978 seqs, 220691566 residues

Footal number of hits satisfying chosen parameters:

Maximum DB seq length: 0

Waximum DB seq length: 30

Maximum Match 08

Maximum Match 1008

Listing first 45 summaries
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US-09-049-190-6

US-09-932-140C-6

US-08-932-140C-7

US-08-932-140C-7

US-08-758-306-365

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                                                                                                      OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Match Length
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Perfect score:
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No. 6190866ris LLP
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Fatent No. 6147056

GENERAL INFORMATION:
APPLICANT: Gilchrest, Barbara A.
APPLICANT: Vaar, Mina
APPLICANT: Eller, Mark
ITILE OF INVENTION: US 60 Locally Applied DNA Fragments
FILE REFERENCE: BU34-68A2
CURRENT APPLICANTION NUMBER: US/09/048,927
CURRENT FILING DATE: 1998-02.26
EARLIER FILING DATE: 1996-06-03
EARLIER FILING DATE: 1996-06-03
EARLIER FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PastSEQ for Windows Version 3.0
EENGTHA: PastSEQ for Windows Version 3.0
EENGTH: PastSEQ for Windows Version 3.0
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Patent No. 6190866

GENERAL INPORMATION:

APPLICANT: Nielsen et al.

TITLE OF INVENTION: Antibacterial Activity

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSE: Woodcock Washburn Kurtz Mackiewicz

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: U.S.A.
US-07-977-284A-59
US-08-256-426B-59
US-08-985-162-444
US-08-985-162-444
US-08-363-55
US-08-363-55
US-08-368-55
US-08-368-55
US-08-368-55
US-09-213-766-29
US-09-213-766-29
US-09-142-218-8
US-09-142-109-21
US-09-422-978-4648
US-09-422-978-4648
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backbone
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backbone
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backbone
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backbone
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backbone
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backbone
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                         ISIS-2560
                                                                              SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,190
                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: John W. Caldwell
REGISTRATION NUMBER: 28,937
REFERENCE/DOCKET NUMBER: 15IS-
TELECOMMUNICATION INFORMATION:
TELEFAX: 215-568-3100
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LOCATION: 5
OTHER INFORMATION: N-ace
OTHER INFORMATION: backb
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LOCATION: 4
OTHER INFORMATION: N-ace
OTHER INFORMATION: backb
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NAME/KEY: Modified-site
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LOCATION: 8
OTHER INFORMATION: N-ace
OTHER INFORMATION: backb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1
OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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& No. 6190866ris LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 9; DB 3; Length 15; ilarity 100.0%; Pred. No. 1.5e+03; Conservative 0; Mismatches 0; Indels
                OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine OTHER INFORMATION: backbone FEATURE:
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OTHER INFORMATION: N-acetyl (2-aminoethyl) glycine
OTHER INFORMATION: backbone
                                                                                                                         N-acetyl (2-aminoethyl) glycine
backbone
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backbone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Peptide Nucleic Acids Having TITLE OF INVENTION: Antibacterial Activity NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/09/049,190
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; Sequence 7, Application US/09049190
; Patent No. 6190866
; GENERAL INFORMATION:
APPLICANT: Nielsen et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: John W. Caldwell
REGISTRATION NUMBER: 28,937
REFERENCE/DOCKET NUMBER: ISIS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09,
                                                                                  NAME/KEY: Modified-site
LOCATION: 11
OTHER INFORMATION: N-ace
OTHER INFORMATION: backb
                                                                                                                                                                                                                                                                                                             NAME/KEY: Modified-site
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 14
OTHER INFORMATION:
OTHER INFORMATION:
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Matches 9; Conserv
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LOCATION: 10
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OTHER INFORMATION: N-acetyl (2-aminoethyl) glycine OTHER INFORMATION: backbone
                                                                                                                                                                                                                         NAME/KEY: Modified-site
LOCATION: 2
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
                                                                                                                                                                                                                                                                                                           NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine.
OTHER INFORMATION: backbone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 7
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine OTHER INFORMATION: backbone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 5
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine OTHER INFORMATION: backbone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 12
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 13
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
'BATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine OTHER INFORMATION: backbone
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OTHER INFORMATION: N-acetyl (2-aminoethyl) glycine OTHER INFORMATION: backbone
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LOCATION: 10
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
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INPORMATION FOR EEQ ID NO: 7 SEQUENCE CHARACTERISTICS: LENGTH: 15 bases TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Modified-site LOCATION: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Modified-site LOCATION: 8
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NAME/KEY: Modified-site
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                                                                                                                                                         LOCATION:
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OTHER INFORMATION: N-(acetyl(2-aminoethyl))-C-lysine-glycine
US-09-049-190-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 2
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine backbone
                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 9; DB 3; Length 15, 100.0%; Pred. No. 1.5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08932140C
; Patent No. 430018
; GENERAL INFORMATION:
APPLICANT: Nielsen et al.
TITLE OF INVENTION: Aptide Nucleic Acids Having
TITLE OF INVENTION: Antibacterial Activity
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: Woodcock Washburn Fup
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
                                                           OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine OTHER INFORMATION: backbone
                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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Septemeber 16, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Microsoft World CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/932
FILING DATE: Septemeber 16, 1
CLASSIFICATION: Septemeber 16, 1
FRIOR APPLICATION: Septemeber 16, 1
FRIOR APPLICATION: Septemeber 16, 1
FRIOR APPLICATION NUMBER: Septemeber 16, 1
ATORNEY/AGENT INFORMATION:
NAME: John W. Caldwell
REGISTRATION NUMBER: 28,937
REFREENCE/DOCKET NUMBER: 151S
TELECOMMUNICATION INFORMATION:
NAME/KEY: Modified-site
                                                                                                                                                          NAME/KEY: Modified-site LOCATION: 15
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Best Local Similarity 100.
Matches 9; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GAGTATGAG 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-932-140C-6/c
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LOCATION: 1
OTHER INFORMATION: N-acetyl (2-aminoethyl)glycine
OTHER INFORMATION: backbone
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OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
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OTHER INFORMATION: N-acetyl (2-aminoethyl)glycine
OTHER INFORMATION: backbone
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OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine OTHER INFORMATION: backbone
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backbone
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backbone
ADDRESSEE: No. 6300318ris LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                    ZIP: 19103
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COMPUTER: 18M PC compatible
COMPUTER: 18M PC-DOS/MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/932,140C
FILING DATE: Septemeber 16, 1997
                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: John W. Caldwell
REGISTRATION UNDRER: 28,937
REFRENCE/DOCKET NUMBER: ISIS.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Modified-site
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NAME/KEY: Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION: N-acetyl (2-aminoethyl) glycine backbone BATURE:
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LOCATION: 7
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine backbone
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OTHER INFORMATION: N-acetyl (2-aminoethyl) glycine backbone
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OTHER INFORMATION: N-acetyl (2-aminoethyl)glycine backbone
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OTHER INFORMATION: N-acetyl (2-aminoethyl)glycine backbone
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OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine backbone
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OTHER INFORMATION: N-acetyl (2-aminoethyl) glycine backbone
  OTHER INFORMATION: N-acetyl (2-aminoethyl) glycine backbone
                                                                                       N-acetyl (2-aminoethyl) glycine backbone
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OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine backbone
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LOCATION: 14
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
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Sequence 7, Application US/08932140C

Patent No. 6300318

GENERAL INFORMATION:
APPLICANT: Nielsen et al.
TITLE OF INVENTION: Peptide Nucleic Acids Having
TITLE OF INVENTION: Ancibacterial Activity
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
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OTHER INFORMATION: N-[acetyl(2-aminoethyl)]-C-
OTHER INFORMATION: lysine-glycine backbone
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LOCATION: 10
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                                             NAME/KEY: Modified-site
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                                                                    LOCATION: 4
OTHER INFORMATION:
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Best Local Similarity
Matches 9; Conserv
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100.0%; Score 9; DB 1; Length 17; 100.0%; Pred. No. 1.5e+03;
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TREATMENT OF DISEASES
ASSOCIATED WITH
INTERLEUKIN-2 RECEPTOR
GAMMA-CHAIN EXPRESSION
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
                                  CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
FATORNEY/AGENT INFORMATION:
NAME: WATCHING, WITCHING, RECISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/132
TELECHOME: (213) 955-0440
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OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ VETSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,306
FILING DATE: December 3, 1996
CLASSIPICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         December 3, 1996
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633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Stinchcomb, Dan T. APPLICANT: McSwiggen, James A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 365:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
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INFORMATION FOR SEQ ID NO: 367:
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TELECOMMUNICATION INFORMATION
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NAME: Warburg, Richard J
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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CITY: Los Angeles
STATE: California
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US-08-758-306-365
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                                  N-acetyl(2-aminoethyl)glycine
backbone
                                                                                                                                                   NAME/KEY: Modified-site
LOCATION: 10
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
OTHER INFORMATION: backbone
                                                                                                                                                                                                                                                                                                                                                                                                  N-acetyl (2-aminoethyl) glycine
backbone
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backbone
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backbone
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backbone
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APPLICANT: Stinchcomb, James A.
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES
TITLE OF INVENTION: ASSOCIATED WITH
TITLE OF INVENTION: INVENTION: ASSOCIATED WITH
TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION
NUMBER OF SEQUENCES: 1379
CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: 35" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ESULT 6
Sequence 365, Application US/08758306
Sequence 165, Applicatio
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OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,306
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633 West Fifth Street
Suite 4700
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LOCATION: 12
OTHER INFORMATION: N-ace
OTHER INFORMATION: backb
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OTHER INFORMATION: 1
OTHER INFORMATION: 1
FEATURE:
LOCATION: 9
OTHER INFORMATION:
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OTHER INFORMATION:
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STATE: California
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Sequence 371, Application US/08758306
Patent No. 5807743
GENERAL INFORMATION:
                RESULT 9
US-08-758-306-371/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 17;
                                                                DB 1; Length 17;
                                                                                                                                            100.0%; Score 9; DB 1; Le 100.0%; Pred. No. 1.5e+03;
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100.0%; Pred. No. 1.5e+0
ative 0; Mismatches
                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 369:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
       1: 17 base pairs
    nucleic acid
BDNESS: single
                                                       Query Match
Best Local Similarity luv...
9; Conservative
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nucleic acid
EDNESS: single
SEQUENCE CHARACTERISTICS
                                                                                                      1 GAGTATGAG 9
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Best Local Similarity
                                                                                                                        GAGTATGAG 7
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                                    linear
                         STRANDEDNESS:
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                                    ;
US-08-758-306-367
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US-08-758-306-369
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Sequence 101, Application US/09287796A
Patent No. 6133246
GENERAL INFORMATION:
APPLICANT: MCKAY, Robert A.
APPLICANT: Dean, Nicholas M.
APPLICANT: Mero, Pam
APPLICANT: Mero, Pam
APPLICANT: George, William A.
TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, James A.
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES
TITLE OF INVENTION: ASSOCIATED WITH
TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR
TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION
NUMBER OF SEQUENCES: 1379
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 9; DB 1; L 100.0%; Pred. No. 1.5e+03;
                                                                                                                                                                                                                                                                                        CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,306
FILING DATE: December 3, 1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFRENCE/DOCKET NUMBER: 212/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELEX: (7-3510
INFORMATION FOR SEQ ID NO: 371:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYRE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                        ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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US-09-287-796-101
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Conservative

1 GAGTATGAG 9

12 GAGTATGAG 4

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TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME FILE REFERENCE: 3053-4052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: McKay, Robert A.
APPLICANT: Dean, Nicholas M.
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett
APPLICANT: Monia, Brett
APPLICANT: Nero, Pam
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
FILE REPERBNCE: ISPH-0318
CURRENT APPLICATION NUMBER: US/09/130,616C
CURRENT FILING DATE: 1998-08-07
EARLIER FILING DATE: 1998-08-07
EARLIER FILING DATE: 1997-08-03
NUMBER OF SEQ ID NOS: 178
SEQ ID NO 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
             TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3; Le
1.5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                  FILE REFERENCE: ISPH-0318
CURRENT APPLICATION NUMBER: US/09/130,616C
CURRENT FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: 08/910,629
EARLIER FILING DATE: 1997-08-03
NUMBER OF SEQ ID NOS: 178
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 9; Best Local Similarity 100.0%; Pred. No. Matches 9; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Synthetic sequence US-09-130-616-101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Synthetic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 102, Application US/09130616C Patent No. 6221850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15, Application US/09105058C Patent No. 6403360 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Dworetzky, Steven
APPLICANT: Gribkoff, Valentin K.
APPLICANT: Levesque, Paul C.
APPLICANT: Little, Wayne A.
APPLICANT: Neubauer, Michael G.
APPLICANT: Yang, Wen-Pin
                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Blanar, Michael A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 GAGTATGAG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-130-616-102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-130-616-102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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APPLICANT: Monia, Brett A.

APPLICANT: Monia, Brett B.

CONTRENT: Moreo, Paris B.

TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS

TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS

TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS

TITLE OF INVENTION NUMBER: US/09/287,796A

CURRENT FILING DATE: 1999-04-07

EARLIER PILING DATE: 1999-08-07

SARLIER PILING DATE: 1990-08-03

SEQ ID NO 102

LENGTH: 20

LENGTH: 20
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APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett
APPLICANT: Nero, Pam
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
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100.0%; Score 9; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 9; Conservative 0; Mismatches 0; Indels
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; FILE REFERENCE: ISPH-0350; CURRENT APPLICATION NUMBER: US/09/287,796A; CURRENT FILING DATE: 1999-04-07; EARLIER FILING DATE: 1998-08-07; EARLIER FILING DATE: 1998-08-07; EARLIER FILING DATE: 1997-08-03; NUMBER OF SEQ ID NOS: 165

NUMBER OF SEQ ID NOS: 165

SEQ ID NOS: 165

LENGTH: 20
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Best Local Similarity 100.0%; Score 9;

Matches 9; Conservative 0; Mismat.

Matches 9; Conservative 0; Mismat.

Best Local Similarity 100.0%; Pred. No.

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GRESULT 11

Sequence 102, Application US/09287796A

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Monia, Brett

APPLICANT: Monia, Brett
                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Synthetic Sequence US-09-287-796-101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 101, Application US/09130616C
Patent No. 6221850
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGTATGAG 17
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us-09-540-843-1.szlm30.rni

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Query Match

Query Match

Dest Local Similarity 100.0%; Score 9; DB 4; Length 20;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Aptroper Similarity 100.0%; Pred. No. 1.5e+03;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Mismatches 0; Indels 0;

Mismatches 0; Indels 0; Gaps 0;

Mismatches 0; Indels 0;

Mismatches 0;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ). OTHER INFORMATION: Description of Artificial Sequence: Forward primer; OTHER INFORMATION: from EST sequence similar to the KvLQT gene US-09-105-058C-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 20;
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: AntiGense Oligonucleotide
CURRENT APPLICATION NUMBER: US/09/105,058C CURRENT FILING DATE: 1998-06-26 PRIOR PELLING DATE: 1997-08-12 NUMBER OF SEQ ID NOS: 28 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 15 LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: January 1, 2004, 00:32:18
Job time : 35.0858 secs
                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 GAGTATGAG 11
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Appl Appl ,, Appl Ay

Sequence 23 Sequence 56

Sequence Sequence Sequence Sequence Sequence Sequence Sequence

Sequence 102, Sequence 15, P Sequence 15, P Sequence 32, P

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sequence on Application US/10122630
sublication No. US20030032610A1
GENERAL INFORMATION:
APPLICANT: Gilchrest, Barbara A.
TITLE OF INVENTION: Mathod to Inhibit Cell Growth Using
TITLE OF INVENTION: Oligonuclectides
FILE REFERRINCE: 0054.1088-018
CURRENT APPLICATION NUMBER: US/10/122,630
CURRENT FILING DATE: 2002-04-12
PRIOR PLILING DATE: 1995-06-06
PRIOR PELING DATE: 1995-06-06
PRIOR FILING DATE: 1996-06-03
PRIOR PELING DATE: 1996-06-03
PRIOR PELING DATE: 1996-06-03
PRIOR PELING DATE: 1996-06-03
PRIOR PELING DATE: 1996-06-03
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-36
PRIOR FILING DATE: 2001-03-31
PRIOR PELING DATE: 2001-03-31
PRIOR PELING DATE: 2001-03-31
PRIOR FILING DATE: 2001-03-31
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US-10-215-112-4205
US-10-215-112-42329
US-10-215-112-10765
US-10-215-112-10891
US-10-098-2638-9340
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100.0%; Score 9; DB 15; I
Best Local Similarity 100.0%; Pred. No. 3.8e+08;
Matches 9; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                        US-09-866-108-5683
US-09-866-108-5684
US-09-866-108-5685
US-09-866-108-5685
US-09-866-108-5687
US-09-866-108-5687
US-09-866-108-5688
US-10-205-309-506
US-09-77-4-809-101
US-09-774-809-102
US-10-128-870-15
US-10-11-685-15
US-10-067-514-32
US-09-815-656-23
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US-09-866-108-5692
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US-09-866-108-5695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
  US-10-122-630-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA
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Sequence 1, Appli
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                                                                                                                                                                                       December 31, 2003, 17:10:00 ; Search time 104.924 Seconds (without alignments) 296.896 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:
                    GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gapop 10.0, Gapext 1.0
Searched: 2263443 seqs, 1730637950 residues

Attornal number of hits satisfying chosen parameters:
Rinimum DB seq length: 0
Aximum DB seq length: 30
Dest-processing: Minimum Match 0*
Maximum Match 100*
Total 
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US-09-866-108-2751
US-09-866-108-2753
US-09-866-108-2753
US-09-866-108-2755
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US-09-866-108-2756
US-09-866-108-2756
US-09-866-108-2756
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                                                                                                                                  OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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                                                    Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
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                                                                                                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                          Run on:
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Sequence 10765, Sequence 37, Apsorption Sequence 4205,

Sequence 4329

Sequence 5694, Sequence 5695,

Sequence 5 Sequence 5 Sequence 5

Sequence Sequence Sequence

Sequence 9340,

Sequence

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Gaps

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1 GAGTATGAG 9

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Length 9; Indels

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APPLICANT: GU, Yizhong
APPLICANT: GU, Yizhong
APPLICANT: GU, Yizhong
APPLICANT: GU, Yizhong
APPLICANT: HANEX, David K.
APPLICANT: HANEX, David K.
APPLICANT: RANK, David R.
APPLICANT: RANK, David R.
APPLICANT: RANK, David R.
APPLICANT: SHANNOW, MARK
TITLE OF INVENTION: WYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-00-6-6
PRIOR FILING DATE: 2000-00-6-6
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PELLING DATE: 2001-01-30
                                                                                                                                                                                                                                        APPLICANT: WISSENBACH, MARGIT
APPLICANT: WISSENBACH, MARGIT
APPLICANT: WOUN, HENRICK
APPLICANT: WONN, HENRICK
APPLICANT: HANSEN, BO
TITLE OF INVENTION: THERAPEUTIC USES OF LNA-MODIFIED OLIGONUCLEOTIDES IN
TITLE OF INVENTION: THERAPEUTIC USES OF LNA-MODIFIED OLIGONUCLEOTIDES IN
TITLE OF INVENTION: THERAPEUTIC USES OF LNA-MODIFIED OLIGONUCLEOTIDES IN
TITLE OF INVENTION: WHERE: US/10/150,779A
CURRENT APPLICATION NUMBER: 60/291,830
PRIOR FILING DATE: 2003-02-07
PRIOR FILING DATE: 2001-05-18
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: DNA oligonucleotide with phosphorothioate backbone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 9; DB 15; Length 12; 100.0%; Pred. No. 1.7e+04;
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Patent No. US20020048800A1
                                                                                                                                                       Sequence 16, Application US/10150779A Publication No. US20030125241A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                 Publication No. US20030125241A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.
nes 9; Conservative
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      12 GAGTATGAG
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10-150-779A-15/c

10-150-779A-15/c

#$Sequence 15, Application US/10150779A

Publication No. US20030125241A1

Publication No. US2004125241A1

PROBLEMAL INFORMATION:

APPLICANT: WOCH, TROELS

APPLICANT: ORUM, HENRICK

APPLICANT: ORUM, HENRICK

APPLICANT: HENRICK

TITLE OF INVENTION: THERABEUTIC USES OF LNA-MODIFIED OLIGONUCLEOTIDES IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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                                                                                                                                                                                                                                                                        APPLICANT: Glichest, Barbara A.
APPLICANT: Glichest, Mark S.
APPLICANT: Glichest, Mark S.
APPLICANT: Hart.
APPLICANT: Faller, Mark S.
TITLE OF INVENTION: Method to Inhibit Cell Growth Using
TITLE OF INVENTION: Oligonucleotides
FILE REFERENCE: 00541088-018.
CURRENT APPLICATION NUMBER: US 109/540,843
PRIOR APPLICATION NUMBER: PCT/US01/10162
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Synthetic DNA Fragment -10-122-633-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 9;
100.0%; Pred. No.
rative 0; Mismatc
                                                                                                                                                                                    Sequence 1, Application US/10122633
Publication No. US20030032611A1
GENERAL INFORMATION:
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CURRENT FILING DATE: 2002-0-
PRIOR PELING DATE: 2000-03-3:
PRIOR APPLICATION NUMBER: UC
PRIOR APPLICATION NUMBER: PC:
PRIOR PILING DATE: 2001-03-3:
PRIOR APPLICATION NUMBER: PC:
PRIOR FILING DATE: 2010-03-3:
CHARLES PRIOR FILING DATE: 2010-03-3:
SEQ THERE IN NO SEQ ID NOS: 15
SOFTWARE: FREYER 9
TYPE: DNA
OCHANISM: ARTIFICIAL SEQUENC
PEATURE:
CHARLINFORMATION: Synthetic
COTHER INFORMATION: Synthetic
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SEQ ID NO 15
LENGTH: 12
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APPLICANT: RANK, David R.
PEPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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1.7e+04;
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILLING DATE: 2000-05-26
PRIOR PILLING DATE: 2000-00-07
PRIOR PILLING DATE: 2000-00-07
PRIOR PILLING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR PILLING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SSCTWARE: Acomica Sequence Listing Engine
SEQ ID NO 2751
LENGTH: 17
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CURRENT FILING DATE: 2001-05-25
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Patent No. US20020048800A1
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 9, Conservative
                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-2751
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; ORGANISM: Homo sapiens
US-09-866-108-2752
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APPLICANT: PENN, Sharron G.
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: CHEN, Wendheng
APPLICANT: CHEN, Wendheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: WYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
THE REPERBENCE: AECMICA-7
CURRENT APPLICATION NHWER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
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PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR PILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aeomica Sequence Libting Engine SEQ ID NO 2750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR PILING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR PLING DATE: 2000-10-04
PRIOR PLING DATE: 2000-10-04
PRIOR PLING DATE: 2000-09-27
PRIOR PLING DATE: 2000-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR PLING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05
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Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 9; Conservative
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GESULT 6
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GENERAL INFORMATIC
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GAPPLICANT: GU, YI
APPLICANT: GI, YI
APPLICANT: GIN
APPLICANT: GIN
APPLICANT: GIN
CURRENT FILING DATE
CURRENT APPLICATION
CURRENT APPLICATION
PRIOR PILING DATE
PRIOR APPLICATION
PRIOR FILING DATE
PRIOR PAPLICATION
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PARENTAL INFORMATION IN APPLICANT: 01 Y SANDAN SPARTON G. APPLICANT: 02 Y SANTON G. APPLICANT: 03 Y SANTON G. APPLICANT: 04 Y SANTON G. APPLICANT: 05 Y SANDAN SPARTON G. APPLICANT: 05 Y SANDAN SPARTON G. APPLICANT: 05 Y SANDAN SPARTON G. APPLICANT SPARTON G. APPLICANTON NUMBER: 05 06 207, 456

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/0665

PRIOR APPLICATION NUMBER: PCT/US01/0666

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PRIOR APPLICATION NUMBER: PCT/US01/0667

PRIOR APPLICATION NUMBER: PCT/US01/0667

PRIOR APPLICATION NUMBER: PCT/US01/0667

PRIOR PRING PAPIL SANDAN NUMBER: PCT/US01/0667

PRIOR APPLICANTON NUMBER: PCT/US01/0667

PRIOR APPLICANTON NUMBER: PCT/US01/0667

PRIOR PRIOR APPLICANTON NUMBER: PCT/US01/0667

PRIOR APPLICANTON NUMBER: PCT/US01/0667

PRIOR PRING PRING PAPIL SANDAN NUMBER: PCT/US01/0667

PRIOR APPLICANTON NUMBER: PCT/US01/0667

PRIOR APPLICATION NUMBER: PCT/US01/0667

PRIOR APPLICATION NUMBER: PCT/US01/0667
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100.0%; Score 9; DB 9; Lv
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 9; Conservative 0; Mismatches 0;
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Patent No. US20020048800A1
GENERAL INPORMATION:
APPLICANT: GU, Yizhong
APPLICANT: DI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
                                Sequence 2754, Application US/09866108
Patent No. US20020048800A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
US-09-866-108-2754
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APPLICANT: GI, Yizhong
APPLICANT: JI, Yongang
APPLICANT: FIN, Sharron G.
APPLICANT: RANK, David K.
APPLICANT: RANK, David R.
APPLICANT: RANK, Mensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
PILE REFERENCE: AEOMICA-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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100.0%; Score 9; DB 9; Length 17; 100.0%; Pred. No. 1.7e+04;
                                                                                  0; Mismatches
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SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 2753
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2753, Application US/09866108
Patent No. US20020048800A1
                                                                                  9; Conservative
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Best Local Similarity
Matches 9; Conserv
                                Best Local Similarity
Matches 9; Conserv
    Query Match
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RESULT 9

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APPLICANT: RANK, bavid R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYSOIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                    PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR FILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-02-05
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CURRENT FILING DATE: 201-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PLILING DATE: 2000-05-26
PRIOR PLILING DATE: 2000-05-26
PRIOR PLILING DATE: 2000-05-27
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2000-00-27
PRIOR PILING DATE: 2000-00-27
PRIOR PLLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00669
                                                                                          FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
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Patent No. US20020048800A1
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APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-2756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 GAGTATGAG 11
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Best Local Similarity
Matches 9; Conserv
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APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: HANZEL, David R.
APPLICANT: HANZEL, David R.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REPERENCE: AEONICA-7
CURRENT APPLICATION NUMBER: US 60/207, 456
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-06-26
PRIOR PILING DATE: 2000-06-26
PRIOR PILING DATE: 2000-06-26
PRIOR PILING DATE: 2000-06-26
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PLICANT: SHANNON, MATK
TLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
LE REFERENCE: AEOMICA-7
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1.7e+04;
                                                                                                       CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR PLLING DATE: 2001-05-26
PRIOR PLLING DATE: 2000-05-26
PRIOR PLLING DATE: 2000-06-26
PRIOR PLLING DATE: 2000-09-27
PRIOR PLLING DATE: 2000-09-27
PRIOR PLLING DATE: 2000-09-27
PRIOR PLLING DATE: 2001-01-30
PRIOR PLLING DATE: 2001-01-30
PRIOR PLLING DATE: 2001-01-30
PRIOR PLLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PLLING DATE: 2001-01-30
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Patent No. US20020048800A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 9; Conservative
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PRIOR PELING DATE:
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APPLICANT: McSwiggen, James
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Alzheimer's Disease Using
TITLE OF INVENTION: RNA Interfering RNA
FILE REPERENCE: 900/033
FILE REPERENCE: 900/033
CURRENT APPLICATION NUMBER: US/10/205,309
CURRENT FILING DATE: 2002-10-25
NUMBER OF SEQ ID NOS: 674
SEQ ID NOS: 674
SEQ ID NO 181
LENGTH: 19
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APPLICANT: Tao, Yuan-Xiang
TITLE OF INVENTION: Inhibition of interaction of PSD93 and
TITLE OF INVENTION: Inhibition of interaction of PSD93 and
TITLE OF INVENTION: PSD95 with nNOS and NMDA receptors
FILE REPERENCE: 01107.00130
CURRENT APPLICATION NUMBER: US/09/853,895
CURRENT APPLICATION NUMBER: 06/242590
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-05-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                              Length 17;
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100.0%; Score 9; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 9; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFFTARE: Acomica Sequence Listing Engine SEQ ID NO 2758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 181, Application US/10205309
Publication No. US20030190635A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09853895
Patent No. US20020045590A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-2758
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US-09-853-895-1/c
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US-10-205-309-181
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APPLICANT: JI, Yonggang
APPLICANT: PENN, Shartron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: RANK, David R.
APPLICANT: RANK, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
THER REPERBNUE. AEDMICA-7
CURRENT APPLICATION WHERE: 2001-05-25
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100.0%; Pred. No. 1.7e+04;
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                          PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR FILING DATE: 2001-01-30
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PRIOR PELING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PELING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR PRILING DATE: 2001-02-05
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/206,359
PRIOR APPLICATION NUMBER: US 60/206,359
PRIOR PILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00667
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PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00661
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SEQ ID NO 2757
LENGTH: 17
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Patent No. US20020048800A1
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/sinA sense
US-10-205-309-181
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100.0%; Score 9; DB 13; Length 19;
Best Local Similarity 77.8%; Pred. No. 1.7e+04;
Matches 7; Conservative 2; Mismatches 0; Indels
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters:

Phinimum DB seq length: 0

Waximum DB seq length: 30

Opost-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Patent: WO 0198137-A 169 27-DEC-2001;
THIRD WAVE TECHNOLOGIES, INC. (US)
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/note="Synthetic bNA Fragment"

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Molecular Engines Laboratories (FR)
Location/Qualifiers
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AX673343
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
Patent: WO 03025177A 179 27-WAR-2003;
Molecular Engines Laboratories (FR)
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Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
Patent: WO 03025177-A 3623 27-MAR-2003;
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/db_xref="taxon:9606"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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       100.0%; Score 9; DB 6; Length 17; 100.0%; Pred. No. 1.8e+05; tive 0; Mismatches 0; Indels
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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Sequence 3869 from Patent WO03025175.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/mol_type="genomic DNA"
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AX732235.1 GI:30511578
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Bachmanov, A.A., Beauchamp, G.K., Chatterjee, A., de Jong, P.J., Li, S., Li, X., Ohmen, J.D., Reed, D.R., Ross, D. and Tordoff, M.G. Gene and sequence variation associated with sensing carbohydrate compounds and other sweeteners

Patent: WO 0183749-A 48 08-NOV-2001;

WARNER-LAMBERT COMPANY (US); The Monell Chemical Senses Center
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Cohen, D., Chumakov, I. and Blumenfeld, M.
Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
Patent: US 6537751-A 6304 25-MAR-2003;
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Sequence 200 from Patent WO0178894.
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Sequence 484 from Patent WO0183749.
AX298850
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/db_xref="taxon:10095"
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/organism="Mus sp."_
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Unclassified.
1 (bases 1 to 20)
Mehtali,M. and Sorg,T.
Transdominant TAT variants of the human immunodeficiency virus Patent: US 6284252-A 6 04-SEP-2001;
Location/Qualifiers
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Mehtali,M. and Sorg,T.
TAT transdominant variants from human Immunodeficiency virus
Patent: EP 0614980-A 6 14-SEP-1994;
TRANSCENE SA (FR)
Other publication CA 2112652 940705
Other publication JP 6234791 940823
Other publication AU 5280393 940714
Other publication AU 688441 960502
Other publication AU 688441 960502
Other publication AU 689491 960502
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Sequence 6304 from patent US 6537751.
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Sequence 6 from patent US 6284252.
AR166936.1 GI:16243331

    .20
    /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

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A39511.1 GI:2295829
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FIGURE 6 a 4 c

GOVERN MATCH 100.09

COMPACT FOR SIMILATITY 100.09

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us-09-540-843-2.szlm30.rge

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
Matanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
and Soeda,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (04-AUG-2001) Akira Horii, Tohoku University School of Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai, Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp, Tel:81-22-717-8042, Fax:81-22-717-8047)
Keith, T.

Novel human gene relating to respiratory diseases, obesity, and inflammatory bowel disease
Patent: WO 0178894-A 200 25-OCT-2001;
Genome Therapeutics Corp. (US)
Location/Qualifiers
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Matches 9; Conservative 0; Mismatches 0; Indels
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db xref="taxon:32630"
/noTe="Primer"
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/mol_type="genomic DNA"
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Search completed: December 31, 2003, 17:09:41 Job time : 831.57 secs

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Oligonucleotide se	Melanogenesis asso	Zinc finger protei	Oligonucleotide pr				
SUMMARIES 1 ID	20 AAZ10693	3 AAS14906	25 ACC41655	23 ABH73149	~	23 ABH83668	23 ABH86802	3 ABH95571
% Query Match Length DB	9 2	6	10 2	12 2	12 2	12 2	12 2	12 2
& Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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Result No.		7	e,	4	O S	9	C 7	œ

Eller M;

Yaar M,

WPI; 1999-543520/46 Gilchrest BA,

24   9   100.0   13   23   ABC40316   Oligomucleotide SE   25   9   100.0   13   23   ABC40316   Oligomucleotide SE   26   9   100.0   13   23   ABC40316   Oligomucleotide SE   28   9   100.0   13   23   ABC40315   Oligomucleotide SE   28   9   100.0   13   23   ABC72173   Oligomucleotide SE   28   9   100.0   13   23   ABC72173   Oligomucleotide SE   29   9   100.0   13   23   ABC84891   Oligomucleotide SE   23   9   100.0   13   23   ABC84891   Oligomucleotide SE   24   9   100.0   13   23   ABC84891   Oligomucleotide SE   24   9   100.0   13   23   ABC94893   Oligomucleotide SE   24   24   24   24   24   24   24   2
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p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis; UV-induced hyperprollferative disease; psoriasis; vitiligo; atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging; skin cancer; ss. Oligonucleotide sequence that increases p53 activity in a cell. AAZ10693 standard; DNA; 9 BP 99GB-0006758 98US-0048927 23-NOV-1999 (first entry) (UYBO-) UNIV BOSTON 24-MAR-1999; 26-MAR-1998; GB2336157-A. 13-OCT-1999, Synthetic. AAZ10693; 

cell and reducing DNA fragments useful for increasing p53 activity in a cel susceptibility to UV-induced hyperproliferative diseases

Claim 11; Page 29; 44pp; English

diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging AAZ10692-97 represent DNA fragments that are used for increasing p53 activity in a cell. The oligonuclectides are are UV mimetics and protect cells against subsequent exposure to UV sirradiation or chemicals. The oligonuclectides are useful for increasing p53 activity in a cell, reducing the susceptibility to UV-induced hyperproliferative and reducing susceptibility to skin cancer.

Sequence 9 BP; 3 A; 0 C; 4 G; 2 T; 0 other;

Gaps ö 100.0%; Score 9; DB 20; Length 9; 100.0%; Pred. No. 2.98+08; ive 0; Mismatches 0; Indels Conservative 0

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AAS14906 standard; DNA; 9

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Melanogenesis associated oligonucleotide #2.

(first entry)

Melanin, melanogenic; oligomer; cytostatic; anti-allergic; p53; anti-inflammatory; dermatological; ophthalmological; anti-psoriatic; immunosuppressive; DNA repair; proliferation inhibitor; apoptosis; tumour necrosis factor inhibitor; photoaging; hyperproliferative disease; carcinoma; oxidative stress; skin cancer; allergy mediated inflammation; conjunctivitis; allergic rhinitis; vitiligo; ss

30-MAR-2001; 2001WO-US10162.

31-MAR-2000; 2000US-0540843

(UYBO-) UNIV BOSTON.

Eller M; Gilchrest BA, Yaar M,

WPI; 2001-626338/72.

Inhibiting proliferation of epithelial cells, useful e.g. for treating carcinoma, using specific oligonucleotides that mimic the effects of ultra-violet light

Claim 1; Page 36; 74pp; English.

induce The invention describes inhibition of mammalian epithelial cell proliferation by treating cells with at least one oligonucleotide, or lite fragment. The compounds, which have cytostatic, anti-allergic, anti-inflammatory, dermatological, ophthalmological, anti-pseriatic and immunosuppressive activities, function as 'ultra-violet mimics' to induce DNA repair processes (or a protective response to later exposure to radiation or chemicals), as a proliferation inhibitor, apoptosis inducer or a tumour necrosis factor inhibitor. Probably they mimic products of DNA damage, or processed DNA-damage intermediates, by inducing the p53

The present invention describes a library comprising polypeptides. Bach polypeptide comprises a first or second zinc finger domain. The domains of each polypeptide are identical to a zinc finger domain from a naturally occurring protein and either do not occur in the same naturally occurring protein or occur in the same naturally occurring protein in a different configuration than in the polypeptide. The domains vary among polypeptides. Also described: (1) producing chimaric nucleic acids; (2) generating an artificial zinc finger polypeptide that specifically binds to a target DNA site, and (3) identifying a nucleic acid encoding a zinc finger polypeptide that specifically recognises a target DNA site.

New library comprising polypeptides having zinc finger domains, useful for producing chimeric nucleic acids

WPI; 2003-268344/26.

Claim 40; Page 101; 234pp; English.

ö hyperproliferative states (e.g. psoriasis or precancerous conditions); reduce photoaging, oxidative stress or damage; prevent skin cancer; treat allergically mediated inflammation (atopic or contact dermatitis, allergic thinitis and conjunctivitis); prevent or reduce DNA damage in cells caused by radiation or chemicals; increase melanin production (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to promote apoptosis in epithelial cells that contain damaged DNA. Also oligonuclectides that contain non-hydrolyzable backbones are used to inhibit apoptosis, in response to DNA damage, in epithelial cell. This sequence is melanogenesis associated oligonuclectide #2, a scrambled version of the oligonuclectide shown in AAS14905, one of the oligonuclectide shown in AAS14905, one of the described in the method of the invention. pathway, resulting in transient arrest of cell growth, allowing more time for DNA repair to occur before cell division takes place. The method is used to treat carcinoma but may also be used to: treat other Zinc finger protein DNA-binding domain target sequence SEQ ID NO:202. Gaps Zinc finger domain; zinc finger; zinc finger binding domain; probe; chimeric nucleic acid; library; PCR primer; ss. ö Length 9; Indels Ryu E, Hwang M; 100.0%; Score 9; DB 23; I 100.0%; Pred. No. 2.9e+08; Sequence 9 BP; 3 A; 0 C; 4 G; 2 T; 0 other; 0; Mismatches Kwon Y, ACC41655 standard; DNA; 10 BP. 17-AUG-2002; 2002WO-KR01560. 17-AUG-2001; 2001US-313402P. 22-APR-2002; 2002US-374355P. (first entry) Local Similarity 100. Les 9; Conservative Bae K, Park K, (TOOL-) TOOLGEN INC. 1 TAGGAGGAT 402003016571-A1 21-MAY-2003 27-FEB-2003. especially Synthetic. ACC41655; Query Match Kim J, RESULT 3 ACC41655 ð g

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ABH79033 standard; DNA; 12 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABH00010-ABH99989 and ABMI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
The library can be used for producing chimeric nucleic acids. ACC41551 to ACC41758 and ABR40919 to ABR41015 represent nucleotide and amino acid
                                                                                                     Gaps
                                                                                                                                                                                                                                                                                            Oligonucleotide primer SEQ ID NO 273134 for detecting SNP TSC0003058.
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                           sequences given in the exemplification of the present invention.
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                                                                           100.0%; Score 9; DB 25; Length 10; 100.0%; Pred. No. 2.9e+04;
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                                                 Sequence 10 BP; 3 A; 0 C; 5 G; 2 T; 0 other;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABE9989 and ABI00010-ABE9989 and ABI00010-ABE82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPPO at
                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                 Oligonucleotide primer SEQ ID NO 279026 for detecting SNP TSC0006799.
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABH00010-ABH99989 and ABI00010-ABH89973 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                            Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single nucleotide polymorphisms and cytosine methylation status
                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID 283661; 29pp + Sequence Listing; German.
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                                                                            WO200177384-A2.
                                                 Homo sapiens.
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Gaps

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100.0%; Score 9; DB 23; Length 12; 100.0%; Pred. No. 2.9e+04; trive 0; Mismatches 0; Indels

TAGGAGGAT 11

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed typ.wipo.int/pub/published_pct_sequences.
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(EPIG-) EPIGENOMICS AG.
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE039989, ABF00010-ABE039989, ABF00010-ABE039989 and ABIC0010-ABE03073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                              100.0%; Score 9; DB 23; I 100.0%; Pred. No. 2.9e+04;
                                                                                                                          Sequence 12 BP; 4 A; 0 C; 5 G; 3 T; 0 other;
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Length 12; 0; Indels

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide primer SEQ ID NO 299027 for detecting SNP TSC0018404. onucleotides, useful for diagnosis and cell typing, is detect single nucleotide polymorphisms and cytosine Claim 1; SEQ ID 299027; 29pp + Sequence Listing; German. Berlin K:

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

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Sequence 12 BP; 3 A; 5 C; 0 G; 4 T; 0 other;
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ABI14652 standard; DNA; 12 BP.

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ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
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tive 0; Mismatches 0;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABCO0010-ABE99989, ABH00010-ABH99989 and ABI00010-ABE9989, ABH00010-ABH99989 and SHI00010-ABE9989, ABH00010-ABH99989 and SHI00010-ABE9980 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                         Oligonucleotide primer SEQ ID NO 314625 for detecting SNP TSC0026468
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Berlin K;

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABRIS073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                     This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE09999, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABF80773 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                oligonucleotides, useful for diagnosis and cell typing, in to detect single nucleotide polymorphisms and cytosine
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ABCCO010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABC99989 and ABC00010-ABH89073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligonucleotide primer SEQ ID NO 340374 for detecting SNP TSC0041493.
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designed to detect single nucleotide polymorphisms and cytosine
methylation status
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100.0%; Pred. No. 2.9e+04;
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Search completed: December 31, 2003, 15:08:13 Job time : 261.089 secs

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AZ31629 T. brucei
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC,
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A234679
A23421110Q
TA262604Q
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A2483180
B2596812
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AZ500675.1 GI:10680728
GSS.
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
RESULT 1
AZ500675
LOCUS
DEFINITION
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AZ393773 1M0157B04
AZ387199 1M0146P20
AZ645664 1M0511C13
                                                        ; Search time 1034.09 Seconds (without alignments) 211.530 Million cell updates/sec
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                                                                                                                                                                      33330
       GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                 Gapop 10.0, Gapext 1.0
Searched: 22781392 segs, 12152238056 residues
Ainimum DB seq length: 0
Maximum DB seq length: 30
Post-processing: Minimum Match 08
Maximum Match 108
Listing first 45 summaries
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AZ393773
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                                              Std Error:
                                                 Insert Length: 10000 Std Error:
Plate: 0157 row: B column: 04
Seq primer: CGTTGTAAAACGAGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                organism="Mus musculus"
                                                                                                                                                                                                                                      /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                           /clone="UUGC1M0157B04"
                                                                                                                                                                                                                                                                                     /db xref="taxon:10090"
                                                                                                                                         High quality sequence stop: 20.
Location/Qualifiers
                      Email: ddunn@genetics.utah.edu
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AZ387199.1 GI:10500900
                                                                                                                                                                                                                                                                                                                                   /sex="Male
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory Mouse DNR Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared but was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-GG10 (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AZ393773 20 bp DNA linear GSS 03-OCT-2000 1M0157B04F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0157B04 F, genomic survey sequence.
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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                                                                                                                                                                                                                                                                                                                                 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clome_lib="Mouse 10kb plasmid UTGCIM library"
/note="Vector: PWD42Tv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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tive 0; Mismatches
                      Insert Length: 10000 Std Brror:
Plate: 0339 row: J column: 10
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
                                                                                                                                                                                          organism="Mus musculus"
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University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                            db_xref="taxon:10090"
clone="UUGC1M0339J10"
Email: ddunn@genetics.utah.edu
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high malar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance." Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 309, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA GSS 02-OCT-2000 Mus musculus
Bukaryota; Metacas (hordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metacas (hordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinaes 1 to 21)
1 (bases 1 to 21)
1 (bases 1 to 22)
1 (bases 1 to 21)
1 (bases 2)
1 (bases 2)
1 (basen, Barber, M., Mesnen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts AZ387199
1M0146P20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic from the Jackson /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-" Gaps /clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jack ö 88.9%; Score 8; DB 28; Length 20; 100.0%; Pred. No. 6e+05; 0; Indels

us-09-540-843-2.szlm30.rst

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil 4732114 [gb]AF129072.1); a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli KL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Bmall: ggapbs-r@mall.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
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mamalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 22)
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
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          84112, uon
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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                                                                                                                                                 Seq primer: CGTTGTAAAACGACGGCCAGTClass: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone="UUGC1M0511C13"
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                                                                                                                                          Insert Length: 10000
Plate: 0511 row: C c
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(http://www.jax.org/resources/documents/dnares/). The DNA
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adaptored DNA was purified and size-selected for a 9.5 to
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with adaptors complementary to the insert adaptors and
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and selected for ampicillin resistance."
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.

1 (Bass 1 to 21)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,

M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone lib="Mouse 10kb plasmid UUGCIM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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                                                       Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                 Insert Length: 10000 Std Error: (Plate: 0146 row: P column: 20 Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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High quality sequence stop: 21.
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/clone="UUGC1M0146P20"
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Tel: 801 585 5606
Fax: 801 585 7177
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15 TAGGAGGA 8
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was but the MNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 k range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi/4732114|gb|AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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L (Dases 1 to 23)

Dunn, D., Aoyagi, A.,

Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished
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2M0096J21F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
                   /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse lokb plasmid UUGCNH library"
/note="Vector: PWD4Zny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Length: 10000 Std Error: 0.00
0096 row: J column ?1
                                                                                                                  Laboratory Mouse DNA Resource

    .23
    /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"

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Location/Qualifiers
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Best Local Similarity 100..
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Fax: 801 585 7177
Email: ddunn@genet
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                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2295174"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/clone lib="NCI_CGAP_Panl"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: Sall;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
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Clone distribution: NCI-CGAP clone distribution information can be
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. Muse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AZ411934 1000 1000 12 bp DNA linear GSS 03-OCT-200 1M0185M09F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0185M09 F, genomic survey sequence.
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Pred. No. 6.2e+05;
                     found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Insert Length: 10000 Std Error: 0.00
Plate: 0185 row: M column: 09
Seg primer: CGTTGTAAAACGACGGCCAGT
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100.0%; Pred. No. co.
                                                                                        Trace considered overall poor quality Insert Length: 1010 Std Error: 0.00 Seq primer: -40VP from Gibco High quality sequence stop: 1. Location/Qualifiers

    .22
    /organism="Mus musculus"

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University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0185M09"
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nes 8; Conservative
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Fax: 801 585 7177
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Gaps ö GSS 20-FEB-2001

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwm92 (gil4732114 |gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.,
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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1M0343E24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0343E24 R, genomic survey sequence.
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                                                                                                                                                                                                                                Gape
      /note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
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                                                                                                                                                                Length 24;
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100.0%; Pred. No. 6.3
ive 0; Mismatches
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Seq primer: CACACAGGAAACAGCTATGACC
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/organism="Mus musculus"
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University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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/clone="UUGC1M0343E24"
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AZ503909.1 GI:10685225
                          Directional"
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet:
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Best Local Similarity
Matches 8; Conserv
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11 AGGAGGAT
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AUTHORS
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HNC5-1-C6.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
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Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42Iv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
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/db xref="taxon:9606"
/db xref="cartilage"
/lab host="E.coli DHIO B"
/clone_lib="HNC (Human Normal Cartilage)"
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clone="UUGC2M0096J21"
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Email: sanjay_kumar-1@gsk.com
Seq primer: T7.
Location/Qualifiers
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100.0%;
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GSS 05-OCT-2000

BASE COUNT ORIGIN

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                        Mus musculus (house mouse)
Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Musi
1 (bases 1 to 25)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
                  AZ491057
1M0324I24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0324I24 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                         Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Male"
/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nr; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 801 585 5606.

Fax: 801 585 7177

Email: ddunmogenetics.utah.edu

Insert Length: 10000 5td Error: 0.00

Plate: 0324 row: I column: 24
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University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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Location/Qualifiers
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(bases 1 to 24)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Simmerman, J. and Ecker, J.R.
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ion lines
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                  chemically-competent E. coli Xi10-Gold (Stratagene) cells and selected for ampicillin resistance." 3 c 9 g b t
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Class: TDNA tagged.

Location/Qualifiers
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Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
1010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Far: 858 453 4100 x1752
  and transformed into
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ive 0; Mismatches 0;
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100.0%; Pred. No. 6.3e+05;
tive 0; Mismatches 0;
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Arabidopsis thaliana
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/strain="Columbia 0"
/db_xref="taxon:3702"
  adaptored vector DNA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis Genome
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27 bp mRNA linear EST 06-DEC-2002 E012698-024-021-P06-SP6 MPIZ-ADIS-024-developing root Beta vulgaris E0592300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line
                                                                                                                                                                                                                                                         Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 27)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
                                                                                                                                                                                                                                                                                                                                                                                                                Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 27 Std Brror: 0.00
Plate: 21 row: P column: 06
Seg primer: SP6; CATACGATTAAGGTGACACTATAG.
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100.0%; Pred. No. 6.6
ive 0; Mismatches
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/clone="024-021-P06"
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                     AZ496986 25 bp DNA linear GSS 05-OCT-2000 1M0333H09R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0333H09 R, genomic survey sequence.
                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. 1 (bases 1 to 25)
Dunn,D., Aoyagi,A.; Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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/lab.host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42rv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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100.0%; Pred. No. 6.4e+05;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plate: 0333 row: H column: 09 Seq primer: CACACAGAAACAGCTATGACC Class: plasmid ende stop: 25. High quality sequence stop: 25. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ddunn@genetics.utah.edu
Length: 10000 Std Err
                                                                                                                                                                         Mus musculus (house mouse)
                                                                                                                         AZ496986.1 GI:10673556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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17 TAGGAGGA 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84112.
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source

on 05/19/2004

/tissue\_type="developing root"
/tab host="EMDH10B"
/clone lib="MPDH10B"
/note="Vector: pCMVSPORT6; Site\_1: Sal1; Site\_2: NotI;
/note="vector: pcm, sugar beet, library provided by KWS
/kleinwanzlebener Saatzucth AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation: SP6-Sall-CCACGCGTCCG-Sprime-cDNA-polyA-CC-Notl-77; Note: Sequencing granted in the context of the GABI-Beet project local Pl: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de" 04-SEP-2002 ö BH903668 103141.14.55.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK\_103141.14.55.x, genomic Gaps ö Length 27; 0: Indels DB 13; LO . 6.6e+05; GSS ACCESSION VERSION KEYWORDS

BASE COUNT ORIGIN

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SOURCE

TITLE

COMMENT

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Search completed: December 31, 2003, 19:41:13 Job time : 1038.09 secs
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                                      Eukaryotta, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; rosids; eurosids II, Brassicales; Brassicaceae, Arabidopsis.

(bases 1 to 27)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ480483 28 04-0CT-2000 1M0302J04F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC1M0302J04 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db xref="cacamora" / db xref="cacamora" / db xref="cacamora" / clone="SALK 103141.14.55.x" / clone="SALK 103141.14.55.x" / clone libs-"Arabidopsis thaliana TDNA insertion lines / note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html" 2 c 11 g 6 t
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 28)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Blan, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At1g11590. Class: TDNA tagged.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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                                                                                                                                                                                                                                                                                Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88.9%; Score 8; DB 28; Length 27; 100.0%; Pred. No. 6.6e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Arabidopsis thaliana"
/mol type="genomic DNA"
/strain="Columbia 0"
Arabidopsis thaliana (thale cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
                                                                                                                                                                                                                                                                Contact: Joseph R. Ecker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AZ480483.1 GI:10641548
GSS.
                                                                                                                                                                                                                                                                                                                                                                                          Email: ecker@salk.edu
                        Arabidopsis thaliana
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84112, US
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                                                                                                         REFERENCE
AUTHORS
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KEYWORDS
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TITLE

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Inductible C79214 (MATA RESOURCE (LDE) TOWN TOWN TOWN CHARTEN ASSOCIATION (MATA) WAS CASCALLED TOWN TOWN TOWN CASCALLED (MATA). The DDAR was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwM22 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T1-resistant, F-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'lab_host="E. Coli strain XL10-Gold,
                                                                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0302 row: J column: 04
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Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0302J04"
                                                                                                                                                                                                                                                High quality sequence stop: 28
                                                                                                                                                                                                                                                                                     ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            musculus C57BL/6J
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Best Local Similarity 100.
Matches 8; Conservative
Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TAGGAGGA 8
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Sequence 9560, Ap Sequence 11185, A Sequence 23551, A Sequence 23552, A Sequence 2359, A Sequence 8788, A Sequence 8788, A

Sequence Sequence Sequence 97906, A Sequence 98973, A Sequence 12144, A Sequence 125474, Sequence 125474, Sequence 26, Appl Sequence 31, Appl Sequence 43, Appl Sequence 43, Appl Sequence 26, Appl Sequence 105, Appl Sequence 28, Appl Sequence 28,

US-10-379-836-12 US-10-379-836-13 US-10-027-836-13 US-10-098-2638-960 US-10-098-2638-960 US-10-098-2638-9551 US-10-098-2638-95551 US-10-098-2638-95551 US-10-098-2638-9748 US-10-098-2638-9748 US-10-098-2638-9748 US-10-098-2638-9774 US-10-098-2638-9774 US-10-098-2638-9774 US-10-098-2638-9774 US-10-098-2638-9774 US-10-098-2638-9774 US-10-098-2638-9774 US-10-098-2638-9774 US-10-098-2638-9774 US-10-098-2638-112143 US-10-098-2638-112143 US-10-098-2638-112143 US-10-088-446-3 US-10-104-105-105 US-10-263-872-28 US-10-263-872-28 US-09-999-789-1611 US-09-999-789-1611 US-09-999-789-1611

Sequence 1611, Ap Sequence 1611, Ap Sequence 53, Appl Sequence 67, Appl Sequence 71, Appl

ALIGNMENTS

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US-10-122-630-2
                                                                                                                               December 31, 2003, 17:10:00 ; Search time 104.924 Seconds (without alignments) 296.896 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published Applications NA:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                      Gapop 10.0, organization of dapop 10.0, organization of 2263443 seqs, 1730637950 residues

Frotal number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 04

Maximum Match 1004

Listing first 45 summaries
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                                                                                      nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Gaps
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Sequence 2, Application US/10122630

Sequence 2, Application US/10122630

Publication No. US20030032610A1

GENERAL INFORMATION:
APPLICANT: Gilchrest, Barbara A.
APPLICANT: Gilchrest, Mark S.
APPLICANT: Gilchrest, Mark S.
TITLE OF INVENTION: Method to Inhibit Cell Growth Using
TITLE OF INVENTION: Oligonucleotides
FILE REFERENCE: 0054.1088-018

CURRENT APPLICATION NUMBER: US/10/122,630

CURRENT FILING DATE: 2002-04-12

PRIOR FILING DATE: 1995-06-06

PRIOR APPLICATION NUMBER: US 09/467,012

PRIOR APPLICATION NUMBER: US 09/048,927

PRIOR APPLICATION NUMBER: US 09/540,843

PRIOR PLING DATE: 1996-06-03

PRIOR PLING DATE: 1996-06-03

PRIOR PRIING DATE: 2000-03-31

PRIOR PRING DATE: 2000-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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Sequence 2, Appli Sequence 102, App Sequence 102, App Sequence 12, Appl Sequence 17, Appl Sequence 162, App Sequence 163, App Sequence 164, App Sequence 114, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 13, Appl Sequence 14, Appl Sequence 14, Appl Sequence 15, Appl Sequence 168, Appl Sequence 17, Appl Sequence 186, Appl

15 US-10-122-630-2
3 US-10-122-633-2
3 US-10-222-765-202
3 US-09-882-94-69
3 US-10-340-192-2-7
1 US-09-766-154-19
1 US-09-766-154-19
1 US-09-766-154-163
1 US-09-828-344-163
1 US-09-828-344-164
1 US-09-828-344-163
1 US-10-06-191-104
1 US-10-166-764-13
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US-10-166-764-13

1000.0 1000.0 1000.0 1000.0 1000.0

Sequence 2, Appli Sequence 2, Appli

Description

Query Match Length

Score

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Sequence 22, Application US/10340192
Sequence 22, Application US/10340192
Publication No. US20030170700A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Shang, Jin
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: US/10/340,192
CURRENT FILING DATE: 2003-01-08
NUMBER OF SEQ ID NOS: 88
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2.2
LIBRICANT: 17
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                                                                                                                                                                                                                                                                    APPLICANT: Lyamichev, Victor
APPLICANT: Lyamichev, Victor
APPLICANT: Allawi, Hadim
APPLICANT: Dong, Fang
APPLICANT: Nexi, Bruce
APPLICANT: Nexi, Bruce
APPLICANT: Nexi, Bruce
APPLICANT: Nexi, Parian
TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
FILE REPERBRUCE: PORS-04586
CURRENT APPLICATION Nucleic Acid Accessible Hybridization Sites
FILE REPERBRUCE: 2008-04586
CURRENT FILING DATE: 2001-06-15
NUMBER OF SEQ ID NOS: 334
SOFTWARE: PatentIn version 3.0
SEQ ID NO 169
LENGTH: 16
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                                                                                                                                                  US-09-882-945A-169/c
; Sequence 169, Application US/09882945A
; Publication No. US20030143535A1
; GENERAL INFORMATION:
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; Sequence 97, Application US/10339793
; Publication No. US20030180764A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 100...
9, Conservative
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Best Local Similarity 100.
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CORGANISM: Homo sapiens
US-10-340-192-22
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                                                                                US-10-12-633-2

| Sequence 2, Application US/10122633
| Sequence 2, Application US/10122633
| Publication No. US20030032611A1
| GENERAL INFORMATION:
| APPLICANT: Gilchrest, Barbara A. |
| APPLICANT: Gilchrest, Barbara A. |
| APPLICANT: Taar, Mina |
| TITLE OF INVENTION: Method to Inhibit Cell Growth Using |
| TITLE OF INVENTION: Oligonucleotides |
| TITLE OLIGOnucleotides |
| T
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WE -10-223-765-202

WI Sequence 202, Application US/10223765

The publication No. US20030165997a1

APPLICANT Kim, Jin-Soo

APPLICANT Rim, Jin-Soo

APPLICANT Run, Sung Hee

APPLICANT Run, Sung Do

APPLICANT Run, Sung Do

APPLICANT Run, Eun-Hyun

APPLICANT: Run, Eun-Hyun

APPLICANT: Lang, Moon-Sun

APPLICANT: Lang, Moon-Sun

TILE OF INVENTION: ZINC FINER DOMAIN LIBRARIES

FILE REFERENCE: 12279-005001

CURRENT APPLICATION NUMBER: 06/313,765

CURRENT PILING DATE: 2002-04-22

FRIOR FILING DATE: 2002-04-22

FRIOR FILING DATE: 2001-08-17

NUMBER OF SEQ ID NOS: 305

SOFTWARE: FASTESEQ FOR WINGOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 9; DB 15; L 100.0%; Pred. No. 3.8e+08; ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/122,633

CURRENT FILING DATE: 2002-04-12

PRIOR APPLICATION NUMBER: US 9/540,843

PRIOR FILING DATE: 2000-03-31

PRIOR FILING DATE: 2001-03-30

NUMBER OF SEQ 1D NOS: 15

SOFTWARE: FastSEQ for Windows Version 4.0

SOTTWARE: FastSEQ for Windows Version 4.0

SOTTWARE: PASTSEQ for Windows Version 4.0

SEQ ID NO 2

SEQ ID NO 2

SEQ ID NO 3

TYPE: DNA

ORGANISM: Artificial Sequence
FRATURE:

OTHER INFORMATION: Synthetic DNA Fragment

COTHER INFORMATION: Watches 9; DB 3

Matches 9; Conservative 0; Mismatches
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US-09-828-344-164
| Sequence 164, Application US/09828344
| Sequence 164, Application US/09828344
| Publication No. US20030044979A1
| GENERAL INFORMATION:
| APPLICANT: C. Frank Bennett
| APPLICANT: Jacqueline Wyatt
| TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPID SCRAMBLASE I EXPRESSION
| FILE REPERRACE: RTS-0147
| CURRENT APPLICATION NUMBER: US/09/828,344
| CURRENT FILING DATE: 2001-04-06
| NUMBER OF SEQ ID NOS: 176
| SEQ ID NO 164
| LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: C. Frank Bennett

PAPLICANT: Jacqueline Wyatt

TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPID SCRAMBLASE I EXPRESSION
FILE REFERENCE: RIS-0147
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                                                                                                                                                                                        Length 20;
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                                                                                          FEATURE:
, OTHER INFORMATION: Antisense Oligonucleotide
US-09-828-344-162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Antisense Oligonucleotide US-09-828-344-163
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CURRENT FILING DATE: 2001-04-06
NUMBER OF SEQ ID NOS: 176
SEQ ID NO 163
LENGTH: 20
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; Sequence 163, Application US/09828344
; Publication No. US20030044979A1
; GENERAL INFORMATION:
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    SEQ ID NO 162
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
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APPLICANT: Lynx Therapeutics, Inc.
APPLICANT: Shang, Jin
APPLICANT: Shang, Jin
APPLICANT: Bowen, Benjamin
TITLE OF INVENTION: GENES AFFECTED BY CHOLESTEROL TREATMENT AND DURING ADIPOGENESIS
FILE REPERENCE: 37-00310018
CURRENT APPLICATION NUMBER: US/10/339, 793
CURRENT FILING DATE: 2003-01-08
NUMBER OF SEQ ID NOS: 443
SOFTWARE: Patentin version 3.1
SEQ ID NO 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 162, Application US/09828344
Publication No. US20030044979A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPID SCRAMBLASE I EXPRESSION
FILE REPREBUCE: RTS-0147
CURRENT PAPLICATION NUMBER: US/09/828,344
CURRENT FILING DATE: 2001-04-06
NUMBER OF SEQ ID NOS: 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 19, Application US/09766154

Sequence 19, Application US/09766154

OGENERAL INFORMATION:

GAPLICANT: Patience, Clive
TITLE OF INVENTION: Swine Defective for Transmission of Porcine Endogenous
TITLE OF INVENTION: Swine Defective for Transmission of Porcine Endogenous
TITLE OF INVENTION: Retrovirus and Uses Thereof
FILE REFERENCE: 61750-311
CURRENT APPLICATION NUMBER: US, 09/766,154
CURRENT PILING DATE: 2001-01-19
CURRENT PILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-02-16
PRIOR APPLICATION NUMBER: U.S. 60/177003
PRIOR PLING DATE: 2000-01-19
ONUMBER OF SEQ ID NOS: 33
CMUMBER OF SEQ ID NOS: 33
CMUMBER OF SEQ ID NOS: 21
LENGTH: 20
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OTHER INFORMATION: Bequence used in amplification of PERV-sequences.

OTHER INFORMATION: sequence used in amplification of PERV-sequences.
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                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                               TYPE: DNA
CORGANISM: Homo sapiens
US-10-339-793-97
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TAGGAGGAT 10
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US-09-828-344-162
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APPLICANT: D'Andrea, Alan
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS OF CANCER SUSCEPTIBILIT
TITLE OF INVENTION: DEFECTIVE DNA REPAIR MECHANISMS AND TREATMENT THEREOF
FILE REFERENCE: 7032/2055
CURRENT APPLICATION NUMBER: US/10/165,099
CURRENT FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 09/998,027
PRIOR APPLICATION NUMBER: US 60/245,756
PRIOR APPLICATION NUMBER: US 60/245,756
NUMBER OF SEQ ID NOS: 352
SOFTWARE: PATENTIAN OFFE: 2000-11-03
NUMBER OF SEQ ID NOS: 352
SOFTWARE: PATENTIAN OFFE: 2000-11-03
NUMBER OF SEQ ID NOS: 352
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Publication No. US20030204075A9
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REPERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                 , OTHER INFORMATION: Description of Artificial Sequence: PCR Primer U_{S-10-160-764-17}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 21;
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                        CURRENT APPLICATION NUMBER: US/10/160,764
CURRENT FILING DATE: 2002-05-31
FRIOR APPLICATION NUMBER: 60/294,766
PRIOR APPLICATION NUMBER: 60/348,909
FRIOR PILING DATE: 2001-10-22
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO: 17
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 9; 100.0%; Pred. No.
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PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 341, Application US/10165099
Publication No. US20030188326A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 9; Conservative
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FILE REFERENCE: 22542-008
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                                                                                                                                                                                                                        APPLICANT: William Gaarde
APPLICANT: William Gaarde
APPLICANT: William Gaarde
APPLICANT: Andrew T. Watt
FILE PER INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSIC
FILE REFERENCE: RTS-0274
CURRENT APPLICATION NUMBER: US/10/006,191
CURRENT APPLICATION NUMBER: US/10/12-10
NUMBER OF SEQ ID NOS: 153
SEQ ID NO 104
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APPLICANT: Chalifoux, Maryse
APPLICANT: Wang, Yang
APPLICANT: Kuzma, Monika Maria
APPLICANT: Gilley, Angela Patricia
TITLE OF INVENTION: Compositions and Methods of Increasing Stress Tolerance
TITLE OF INVENTION: in Plants
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"Dublication No. US20030027136A1

"GENERAL INFORMATION:

A PPLICANT: Goronia, Myand, Cornelia M.

TITLE OF INVENTION: RHEUMATOID ARTHRITIS MARKERS

TITLE OF INVENTION: RHEUMATOID ARTHRITIS MARKERS

FILE REPERENCE: 07039-221001

CURRENT APPLICATION NUMBER: US/09/816,814

CURRENT FILING DATE: 2001-03-23

WINWHER OF SEQ ID NOS: 23

WINWHER PEST OF SEQ FOR WINDOWS Version 4.0
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. 3.6e+04;
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Publication No. US20030144223A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Matches 9; Conservative
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Query Match 100.0%; Score 9; DB 13; Length 23; Best Local Similarity 100.0%; Pred. No. 3.6e+04; Matches 9; Conservative 0; Mismatches 0; Indels.
                         PRIOR PLING DATE: 2000-04-20
PRIOR PLING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-09-28
PRIO
APPLICATION NUMBER: US 60/198,676
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December 31, 2003, 11:36:21; Search time 644.443 Seconds (without alignments) 444.364 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Thinkum DB seq length: 0
Aximum DB seq length: 30
Set-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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09980559 on 05/19/2004
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Pred. No.

PAT 29-OCT-2001 BD083254 Human mat AX470905 Sequence AX62413 Sequence AX624189 Sequence AX629189 Sequence AX629189 Sequence AX629189 Sequence AX629189 Sequence AX631580 Sequence AX631580 Sequence AX6373600 Sequence AX573600 Sequence AX573600 Sequence AX573602 Sequence AX573603 Sequence AX573603 Sequence AX573604 Sequence AX573604 Sequence AX018746 Sequence AX018748 Sequence AX018748 Sequence AX13073 Sequence AX268755 Sequence AX268759 Sequence AX268753 Sequence AX638053 Sequence 177317 Sequence 24 177620 Sequence 32 AR002583 Sequence LPS activ Human mat Sequence Sequence Sequence AX377250 Sequence AX587123 Sequence AX637888 Sequence score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. linear DNA Gilchrest, B.A., Yaar, M. and Eller, M. Use of locally applied dna fragments Patent: WO 01/4342-A 3 11-OCT-2001; PRUSTEES OF BOSTON UNIVERSITY (US) ALIGNMENTS SUMMARIES AX268755 7 bp Sequence 3 from Patent WO0174342. AX268755 GI:16541827 AR285099 AX018746 AX523264 AR082813 AR088823 AX018748 AX343036 AR041154 AR082814 synthetic construct synthetic construct artificial sequences. Length Query Score DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL RESULT 1 AX268755 LOCUS Result õ

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Nielsen, P.E. and Good, L.
Antibiotic-free bacterial strain selection with antisense molecules
Patent: WO 02079467-A 7 10-OCT-2002;
Koebenharns Univesitet (DK)
Location/Qualifiers
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="synthetic antisense oligonucleotide"
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               100.0%; Score 7; DB 6; Lilarity 100.0%; Pred. No. 4.5e+09; Conservative 0: Mismathhi.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7 from Patent W002079467.
AX573597
AX573597.1 GI:27551267
                                                                                                                                                                       AX377258 10 bp
Sequence 20 from Patent WO0212562.
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
1 3 c 0 g
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artificial sequences.
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7; Conservative
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Best Local Similarity
Matches 7; Conserv
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AX573597/c
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AX377258/c
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VERSION
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="texcn:32630"
/note="Synthetic DNA Fragment"
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. 5.8e+09;
                                                                                                                  100.0%; Score 7; DB 6; Le
larity 100.0%; Pred. No. 5.8e+09;
Conservative 0; Mismatches 0;
                       /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Synthetic DNA Fragment"
0 c 2 g 2 t
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DD003254.1 GI:22628864

JP 200137293-A/175.

Homo sapiens (human)

Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 10)

Matsushima, K., Hashimoto, S., Suzuki, T. and Nagai, S.

Human matured/activated dendritic cell expression genes

Patent: JP 200137293-A 175 27-NOV-2001;

JAPAN SCIENCE AND TECHNOLOGY CORP

OS Homo sapiens (human)

PN JP 2001327293-A/175

PD 27-NOV-2001

PF 22-MAY-2000 JP 2000150562

PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI, SHIGENORI PI
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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webthod for determining skin stress or skin ageing in vitro
Patent: Wo Cdesormining skin stress or skin ageing in vitro
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/mol_type="genomic DNA"
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/mol_type="genomic DNA"
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LPS activated human monocyte expressing genes.
BD007857
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1 (Dases 1 to 10)

Matsushima, K., Hashimoto, S. and Suzuki, T.

Matsushima, K., Hashimoto, S. and Suzuki, T.

Pag activated human monocyte expressing genes

Patent: JP 20106999-A 133 21-MAR-2001;

DAPAN SCIENCE AND TECHNOLOGY CORP

OS Homo sapiens (human)

PD 21-MAR-2001
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5/09, CO7K14/47, CO7K16/18, GO1N33/50, GO1N33/53/ /A61K45/00, PC
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/mol_type="genomic DNA"
/mol_bxref="taxon:32630"
/note="Peptide nucleic acid SP4"
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    /organism="Homo sapiens"

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JP 2001069993-A/133.
Homo sapiens (human)
Homo sapiens
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artificial sequences.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Method for determining homeostasis of the skin
Patent: WO 02053714-A 3223 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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Sequence 2615 from Patent WO02053774.
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/mol_type="genomic DNA"
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 1375 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Sequence 3821 from Patent W002053774.
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p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis; UV-induced hyperproliferative disease; psoriasis; vitiligo; atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;
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(c) 1993 - 2003 Compugen Ltd.
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99GB-0006758 98US-0048927 skin cancer; ss. 24-MAR-1999; 26-MAR-1998; GB2336157-A. 13-OCT-1999.

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SUMMARIES

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AAS14907 AAS14911 AAZ10692 AAS14905 AAZ78995 AAZ86425

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Oligonucleotide se

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Description

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PT Susceptibility to UV-induce XX Claim 11; Page 30; 44pp; En XX Cativity in a cell. The oligonucleot cells against subsect chemicals. The oligonucleot chemicals. The oligonucleot chemicals. The oligonucleot chemicals. The oligonucleot in a cell, reducing the susceptibility axis and reducing susceptibility axis and reducing susceptibility axis and reducing susceptibility. The oligonucleot in a cell, reducing the susceptibility axis and reducing susceptibility. The oligonucleot in a cell, reducing the susceptibility axis and reducing susceptibility. The oligonucleot oligo

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fragments useful for increasing p53 activity in a cell and reducing
                                                     susceptibility to UV-induced hyperproliferative diseases
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Claim 11; Page 30; 44pp; English.

AAZ10692-97 represent DNA fragments that are used for increasing p53 activity in a cell. The oligomucleotides are are UV mimetics and protect cells against subsequent exposure to UV-irradiation or chemicals. The oligomucleotides are useful for increasing p53 activity in a cell, reducing the susceptibility to UV-induced hyperproliferative diseases, treating psociasis, vitiligo, atopic dermatitis, allergic rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging and reducing susceptibility to skin cancer.

Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 other;

; 0 Length 7; Indels 100.0%; Score 7; DB 20; I 100.0%; Pred. No. 3.7e+08; ö 0; Mismatches

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AAS14907 standard; DNA; 7 BP.

(first entry)

Melanogenesis associated oligonucleotide #3.

Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53; anti-inflammatory; dermatological; ophthalmological; anti-psoriatic; anti-inflammatory; dermatological; proliferation inhibitor; apoptosis; tumour necrosis factor inhibitor; photoaging; hyperproliferative disease; carcinoma; oxidative stress; skin cancer; allergy mediated inflammation; conjunctivitis; allergic rhinitis; vitiligo; ss.

30-MAR-2001; 2001WO-US10162.

31-MAR-2000; 2000US-0540843

Eller M;

Inhibiting proliferation of epithelial cells, useful e.g. for treating carcinoma, using specific oligonuclectides that mimic the effects of ultra-violet light -Claim 1; Page 36; 74pp; English.

The invention describes inhibition of mammalian epithelial cell proliferation by treating cells with at least one oligonucleotide, or lite fragment. The compounds, which have cytostatic, anti-allergic, anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and immunosuppressive activities, function as 'ultra-violet mimics' to induce DNA repair processes (or a protective response to later exposure to radiation or chemicals), as a proliferation inhibitor, apoptosis inducer or a tumour necrosis factor inhibitor. Probably they mimic products of DNA damage, or processed DNA-damage intermediates, by inducing the p53

Inhibiting proliferation of epithelial cells, useful e.g. for treating carcinoma, using specific oligonucleotides that mimic the effects of altra-violet light

Claim 1; Page 38; 74pp; English

Eller M;

Gilchrest BA, Yaar M, (UYBO-) UNIV BOSTON.

WPI; 2001-626338/72.

carcinoma,

30-MAR-2001; 2001WO-US10162 31-MAR-2000; 2000US-0540843

11-OCT-2001.

pathway, resulting in transient arrest of cell growth, allowing more time for DNA repair to occur before cell division takes place. The method is especially used to treat carcinoma but may also be used to: treat other hyperproliferative states (e.g. posoriasis or precancerous conditions); reduce photoaging, oxidative stress or damage; prevent skin cancer; treat allergically mediated inflammation (atopic or contact dermatitis, allergically mediated inflammation); prevent or contact dermatitis, cells caused by radiation or chemicals; increase melanin production chromote apoptosis in epithelial cells (e.g. for treating vitiliago), and to promote apoptosis in epithelial cells that contain damaged DNA. Also oligonucleotides that contain non-hydrolyzable backbones are used to inhibit apoptosis, in response to DNA damage, in apithelial cell. This sequence is melanogenesie associated oligonucleotide #3, a truncated version of the oligonucleotide shown in AS14906, one of the oligonucleotides used to inhibit mammalian epithelial cell ö Melanin, melanogenic, oligomer; cytostatic, anti-allergic; p53; anti-inflammatory; dermatological; ophthalmological; anti-psoriatic; anti-inflammatory; dermatological; ophthalmological; anti-psoriatic; tumunosuppressive; DNA repair; proliferation inhibitor; apoptosis; tumour necrosis factor inhibitor; photoaging; hyperproliferative disease; carcinoma; oxidative stress; skin cancer; allergy mediated inflammation; conjunctivitis; allergic rhinitis; vitiligo; ss. Gaps ö 100.0%; Score 7; DB 23; Length 7; 100.0%; Pred. No. 3.7e+08; Indels oligonucleotides used to inhibit mammalian epithelial ce proliferation, described in the method of the invention Melanogenesis associated oligonucleotide #7. Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 other; 0; Mismatches /note= "Phosphorylated" Location/Qualifiers AAS14911 standard; DNA; 7 BP /mod\_base= (first entry) Local Similarity 100. nes 7; Conservative \*tag= 1 AGTATGA 7 AGTATGA 7 WO200174342-A2 Key modified\_base 14-FEB-2002 Synthetic. AAS14911; Query Match RESULT 3 AAS1491 ò g

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The invention by treating cells with at least one oligonucleotide, or its fragment. The compounds, which have cytostatic, anti-allergic, canti-inflammantory, dermatological, ophthalmological, anti-psoriatic and immunosuppressive activities, function as 'ultra-violet mimics' to induce to manusouppressive activities, function as 'ultra-violet mimics' to induce to radiation or chemicals), as a proliferation inhibitor, apoptosis inducer or a tumour necrosis factor inhibitor. Probably they mimic products of at the box of the processed DNA-damage intermediates, by inducing the p53 pathway, resulting in transient arrest of cell growth, allowing more time for DNA repair to occur before cell division takes place. The method is ceptally used to treat carcinome but may also be used to: treat other hyperproliferative states (e.g. psoriasis or precancerous conditions); cells caused bhotoaging, oxidative stress or damage; prevent skin cancer; treat allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in cells caused by radiation or chemicals; increase melanin production (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to promote apoptosis, in response to DNA damage in epithelial cells that contain damaged DNA. Also oligonucleotides that contain non-hydrolyzable backbones are used to inhibit mammalian epithelial cell the invention.

Colls caused by radiated to inhibit mammalian epithelial cell colligence is melanogenesis associated oligonucleotide #7, one of the proliferation, described in the method of the invention.
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      describes inhibition of mammalian epithelial cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotide sequence that increases p53 activity in a cell.
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AAZ10692-97 represent DNA fragments that are used for increasing p53

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Melanin, melanogenic, oligomer; cytostatic; anti-allergic; p53; anti-inflammatory; dermatological; ophthalmological; anti-psoriatic; immunosuppressive; DNA repair; proliferation inhibitor; apoptosis; tumour necrosis factor inhibitor; photoaging; hyperproliferative disease; carcinoma; oxidative stress; skin cancer; allergy mediated inflammation; conjunctivitis; allergic rhinitis; vitiligo; ss.
                                                                        diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging and reducing susceptibility to skin cancer.
                   protect cells against subsequent exposure to UV-irradiation or chemicals. The oligonucleotides are useful for increasing p53 activity in a cell, reducing the susceptibility to UV-induced hyperproliferative
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activity in a cell. The oligonucleotides are are UV mimetics and
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                                                                                                                                                                                  100.0%; Score 7; DB 20; Length 9; 100.0%; Pred. No. 2.9e+08;
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/note= "Optionally phosphorylated"
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                                                                                                                                              Sequence 9 BP; 3 A; 0 C; 4 G; 2 T; 0 other;
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98US-0090076

19-JUN-1998;

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pathway, resulting in transient arrest of cell growth, allowing more time for DNA repair to occur before cell division takes place. The method is especially used to treat carcinoma but may also be used to: treat other hyperproliferative states (e.g. poriasis or precancerous conditions); reduce photoaging, oxidative stress or damage; prevent skin cancer; treat allergically mediated inflammation (atopic or contact dermatitis, allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in cells caused by radiation or chemicals, increase melanin production (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to promote apoptosis in epithelial cells that contain damaged DNA. Also
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CC for DNA repair to occur before compactably used to treat carcino compactable caused by radiation or che (pigmentation) in epithelial colloque apportation or che (pigmentation) described in the colloque apportation of the proliferation, described in the colloque apportation of the proliferation, described in the colloque apportation apportation apportation of the proliferation apportation of the proliferation apportation of the proliferation apportation and apportation apporta
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Expression) tags used to identify mRNA transcripts encoding the immunostimulatory cofactor proteins which are preferentially or immunostimulatory cofactor proteins which are preferentially or differentially expressed in monocyte-derived dendritic cells compared with monocytes. Some of the transcripts correspond to known genes or stress (expressed sequence teas) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while cother transcripts correspond to novel genes. Autigen-presenting cell (APC)-associated costimulatory factors play an important role in the other transcripts correspond to novel genes. Autigen-presenting cell activation of the cytotoxic immune response, particularly against tumour cells rumour antigen presentation via the MHC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone insufficient to activate a robust cytotoxic immune response that can large the tumour cells, immunostimulatory cofactors also being required for efficient activation of cytotoxic immune response that can lyse the tumour antigen for cytotoxic immune response that can lyse the tumour antigen for cytotoxic immune response, particularly sequences identified using the SAGE tags have several potential uses.

Complex) and subvidisation of cytotoxic immune response, particularly against a tumour antigen; to modulate the genotype of an APC; to screen for agents that modulate expression of diseases related to abnormal cappensis and monitoring of diseases related to abnormal cappensis not been genes. Detection of the dendritic cells on taining them are used in quiet encoded proteins and APC-associated costimulatory factors ensures adequate antigen presentation of antigen-specific effector cells) and vectors containing them are used in gene therapy. Co-administration of cell growth factors and secretion of co-stimulatory signals, migration of cell-rich munum effector cells.
                                                                                                                                                                                                                                                                                                                  Isolated polynucleotides differentially expressed in antigen-presenting cells, useful in gene vaccines against cancer -
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100.0%; Pred. No. 5.7e+04;
tive 0; Mismatches 0;
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                   98US-0090077.
98US-0090078.
98US-0090079.
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                                                                                                                                                                                           SHANKARA S.
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19-JUN-1998;
19-JUN-1998;
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08-DEC-1998;
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us-09-540-843-3.szlm30.rng

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transcripts that are preferentially transcribed in the metastatic breast transcripts that are preferentially transcribed in the metastatic breast trumour cells).

AA283942 to AA286677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour cells).

AA283942 to AA286677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected call types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines, for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and treatment of cancer -
                  Human, metastatic breast tumour tissue, breast cancer, tag; primer, non-metastatic breast tumour tissue, gene therapy; anticancer; antimetastatic; vaccine, diagnosis, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      isolate populations of educated, antigen-specific i
3, e.g. cytotoxic T lymphocytes, and these used for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 7; DB 21; Length 10; 100.0%; Pred. No. 5.7e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10 BP; 5 A; 0 C; 3 G; 2 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 208; 219pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH32760 standard; cDNA; 10 BP.
                                                                                                                                                                                                                                                        98US-0089997.
                                                                                                                                                                                                                                                                                        98US-0090040.
                                                                                                                                                                                                   99WO-US13647
                                                                                                                                                                                                                                       98US-0089853
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                       Roberts BL, Shankara S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1mmunotherapy.
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ROBERTS B L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-106079/09.
                                                                                                                                                                                                                                                                                                                                                                                    SHANKARA S.
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effecter cells,
                                                                                                                                                                                                                                                    19-JUN-1998;
19-JUN-1998;
19-JUN-1998;
19-JUN-1998;
                                                                                        Homo sapiens
                                                                                                                            WO9965928-A2
                                                                                                                                                                                                 18-JUN-1999;
                                                                                                                                                                                                                                   19-JUN-1998;
                                                                                                                                                             23-DEC-1999.
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(SHAN/)
                                                                                                                                                                                                                                                                                                                                                (GENZ )
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AAH32760
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The present invention describes an lipopolysaccharide (LPS) activated human monocyte expression gene group consisting of the highest ranking 50 genes of the highest expression among the genes expressed by human monocyte stimulated by LPS in which the CDNA of each gene has the base sequence of (AAH32628 to AAH32677) continuous to the base sequence 5'-CATG-3' nearest to the polyA region. The gene group is useful for the development of new means for the diagnosis and the treament of various human diseases in which human monocyte plays an important role. AAH32628 to AAH32943 represent specifically claimed LPS activated human monocyte expression gene CDNA tags from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   represents an LPS activated human monocyte expression gene cDNA sequence encoding AAB98009, which are given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yeast, Saccharomyces cerevisiae, characterisation, cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification;
                                              Human, LPS, lipopolysaccharide, monocyte expression gene; tag; EST; expressed sequence tag; diagnosis; human disease; treatment; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
              LPS activated human monocyte expression gene cDNA tag SEQ:133.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 7; DB 22; Length 10; 100.0%; Pred. No. 5.7e+04; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (east NORF gene SAGE tag oligonucleotide SEQ ID NO:5675.
                                                                                                                                                                                                                                                                                                                                          LPS activated human monocyte expression gene group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10 BP; 4 A; 0 C; 4 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                       (KAGA-) KAGAKU GLJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                                                                          Claim 10; Page 28; 52pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF38936 standard; DNA; 10 BP.
                                                                                                                                                                                                     28-APR-2000; 2000JP-0131079.
                                                                                                                                                                                                                                       99JP-0195103
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                          WPI; 2001-304369/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linker; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AGTATGA 7
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                                                                                                                                 JP2001069993-A.
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                                                                                                                                                                                                                                       08-JUL-1999;
                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nvention.
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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previoually assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of pression of a NORF genes to antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M2) for identifying human genes which are involved in cell cycle expression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1, and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 10 NORF gene whose expression is affected by the class of the cell cycle. The methods may be used as markers of phases of the cell cycle the cell cycle and for identification of antifungal drugs.

AFRICACE THE CALL OF THE MATER AND THE CALL OF AND THE CALL OF Yeast gene coding sequences comprising NORF genes with serial an of gene expression (SAGE) tags, useful for studying, monitoring affecting phases of the cell cycle -Kinzler Example; Page 202; 419pp; English Velculescu V, Vogelstein B, UNJO ) UNIV JOHNS HOPKINS WPI; 2001-061874/07.

Sequence 10 BP; 4 A; 1 C; 3 G; 2 T; 0 other;

present invention. ÅAF33262 to AAF33267 represent linkers and PCR imers used in the SAGE method, in the exemplification of the present

Gaps . 0 100.0%; Score 7; DB 22; Length 10; 100.0%; Pred. No. 5.7e+04; tive 0; Mismatches 0; Indels Conservative

1 AGTATGA 7

AAF39793 standard; DNA; 10 BP. RESULT 10

AAF39793;

23-MAR-2001 (first entry)

Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6532.

Yeast, Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds. 

Saccharomyces cerevisiae.

WO200077214-A2

21-DEC-2000

14-JUN-2000; 2000WO-US16223

SNINGO NIND ( OFAD)

Jelculescu V, Vogelstein B, Kinzler K;

analysis

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WPI; 2001-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle -

Example; Page 233; 419pp; English.

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previoually assigned open reading frame; or nonnotated ORF) genes.

Comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell comprising adminstering a NORF gene whose expression varies by at cell and (b) between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate by at cell; and (b) monitoring expression of a NORF gene whose cypression varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which man DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1, and (M4) for identifying a candidate drug as a candidate drug as a condidate drug and monitoring expression in the yeast cell with a candidate drug and monitoring expression in the yeast cell with a candidate drug and monitoring expression in the yeast cell with a candidate drug and monitoring expression in the yeast cell with a candidate drug and monitoring expression in the yeast cell with a candidate drug and monitoring expression in the yeast cell with a candidate drug and monitoring expression in the yeast cell with a candidate drug and monitoring expression in the yeast cell with a candidate drug and monitoring expression in the yeast cell with a candidate drug such the cell cycle, the cell cycle as the cell cycle. The methods may be used as markers of phases of the cell cycle. The methods may be used as markers of phases of the candidate drug such and year identification of an antification of a chartifulated drugs which a proper proper pages of drugs which are the cell cycle. The methods may be used to identify course. AAF33268 to AAF44664 represent SACE tags used in the exemplification of the present invention. AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present %XCCCCCCCCCCCCCCCCCCCCCCX

Sequence 10 BP; 4 A; 1 C; 2 G; 3 T; 0 other;

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Gaps ö Length 10; 100.0%; Score 7; DB 22; Length 10 100.0%; Pred. No. 5.7e+04; ive 0; Mismatches 0; Indels Query Match Best Local Similarity 100.

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ð g

AAF40876 standard; DNA; 10 BP. AAF40876; AAF40876

RESULT 11

Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7615.

(first entry)

23-MAR-2001

Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds. 

Saccharomyces cerevisiae

us-09-540-843-3.szlm30.rng

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Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle -
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Target nucleotide; analyte; signal; drug discovery; probe; ss.
                                                                                                                                                                                                                                                                                                                        Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                         AAD44180 standard; DNA; 10 BP.
                                                                    Velculescu V, Vogelstein B,
                               14-JUN-2000; 2000WO-US16223.
                                           99US-0335032.
                                                        (UYJO ) UNIV JOHNS HOPKINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                WPI; 2001-061874/07.
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AGTATGA 9
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       WO200077214-A2
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                                           16-JUN-1999;
                   21-DEC-2000
                                                                                                                                                                                                                                                                                                            invention
                                                                                                                                                                                                                                                                                                                                                                                                                      AAD44180;
                                                                                                                                                                                                                                                                                                                                    Query Match
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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previoually assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a vestression varies as in M1, where a test substance which modifies the expression varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1, and (4) a method (M4) for identifying a candidate drug as a member of a class of fungs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell of at least 10 NORF gene whose expression in a sefected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle. The methods may be used as markers of phases of the cell cycle. The methods may be used to identify and drugs. AAP13268 to AAP44064 represent invention of antifungal drugs. primers used in the SAGE method, in the exemplification of the present Example; Page 272; 419pp; English

Detecting a target nucleotide sequence in an analyte, for use in e.g. drug discovery, comprises using a set of features having oligophosphodiester probes, and subtracting a background signal from an

Sampras NM;

Overman LB,

Luebke KJ,

Lefkowitz SM,

Delenstarr GC, Letkuming Wolber PK;

WOLBER P K.

(SAMP/) S (SAMP/) S (WOLB/) V

OVER/) LUEB/

WPI; 2002-443693/47.

99US-0398399 99US-0398399

17-SEP-1999; 17-SEP-1999;

02-MAY-2002

US2002051973-A1.

Unidentified.

DELENSTARR G C. LEFKOWITZ S M. LUEBKE K J. OVERMAN L B. SAMPRAS N M. SAMPSON J R.

DELE/)

Kinzler K;

Gaps ö 100.0%; Score 7; DB 22; Length 10; 100.0%; Pred. No. 5.7e+04; 0; Indels 0; Mismatches Best Local Similarity 100. Matches 7; Conservative

ö

Probe #3 used to illustrate the method of the invention.

ö probes, and subtracting a background signal from an observed signal to determine the presence and/or amount of the target sequence in the analyte. The method is used to detect the presence and/or amount of a target sequence in an analyte. The method is used for estimating background noise in a nucleic acid hybridisation assay and for validating a test-background feature. The method is useful in chemical, biological medical and diagnostic techniques, and for drug discovery. The present sequence is a probe used to illustrate the method of the invention. amount of a target nucleotide sequence in an analyte. The method comprising: contacting an aliquot of an analyte suspected of containing the target sequence with a set of features comprising oligophosphodiester PNA oligomer; PNA; peptide nucleic acid; polyamide backbone; 88; aminoethylglycine; aeg; aminoethylpryl; aep; aminoethylpyrrolidine; pyr; gene downregulation; bacterial infection; viral infection; cancer; metabolic disease; immunological disorder; PNA-clamping. Gape The invention relates to a method for detecting the presence and/or .. 0 Length 10; 0; Indels 100.0%; Score 7; DB 24; I 100.0%; Pred. No. 5.7e+04; Sequence 10 BP; 5 A; 1 C; 2 G; 2 T; 0 other; 0; Mismatches Peptide nucleic acid (PNA) oligomer #3. Location/Qualifiers Claim 7; Page 19; 35pp; English. AAL44343/c ID AAL44343 standard; DNA; 10 BP. (first entry) Query Match Best Local Similarity 100. 1 AGTATGA 7 1 AGTATGA observed signal Key modified\_base 24-OCT-2002 Synthetic. AAL44343; RESULT 13

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The detection comprises ontesting the nucleic acid array with the sample under stringent hybridisation conditions, subtracting the background along signal from the hybridisation signal to obtain a background corrected hybridisation signal and relating the background corrected hybridisation signal and relating the background corrected hybridisation signal and relating the target nucleic acid in the sample. The method further comprises a labeling step comprising labeling any analyte target nucleic acids present in the sample with a member of a signal producing system prior to contacting the array with the sample. ABK99529-ABK99544 and ABK99549-ABK99578 represent nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a nucleic acid array (I) comprising at least one hybridisation feature and at least one background feature. (I) is useful for detecting the presence of an analyte nucleic acid in a sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; 88; primer; SNP; single nucleotide polymorphism; pancreatitis; pancreatic cancer; Phospholipase A2 group1B; PLAZG1B; gene therapy; haplotype; genotype; chromosome 12q23-q24.1; transgenic; drug screening; ASO; allele specific oligonucleotide; primer extension.
                                                                                                                                                                                                                                        Nucleic acid arrays for qualitatively or quantitatively determining the presence of analyte target nucleic acid in a sample comprises both hybridisation features and background features -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y Match 100.0%; Score 7; DB 24; Length 10; Local Similarity 100.0%; Pred. No. 5.7e+04; hes 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human PLA2G1B ASO primer extension primer 3' end #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10 BP; 5 A; 1 C; 2 G; 2 T; 0 other;
                                                                                                                                                     Sana TR
                                                                                                                                                                                                                                                                                                                               Claim 8; Page 17; 38pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABK47394 standard; DNA; 10 BP
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                    99US-0398399.
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                                                                                                                                                     Delenstarr GC, Wolber PK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                           DELENSTARR G C.
WOLBER P K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kazemi A, Kliem SE,
                                                                                                                                                                                               WPI; 2002-582474/62.
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                                                                                                       (SANA/) SANA T R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the invention
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                    17-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JUN-2002
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                                                              (DELE/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention comprises peptide nucleic acid (PNA) oligomers, where the single units of the oligomers comprise different amino acid backbones selected from any amino acid, such as: including aminoethylglycine (aeg); selected from any aminoethylpyrolidine (pyr). The PNA oligomers of the invention are useful for the downregulation of specific genes by targeting the genes at the mRNA or DNA level. The PNA oligomers are useful for treating bacterial and viral infections, cancer, metabolic diseases and immunological disorders. The PNA oligomers are also useful in PCR monitoring/modulation by PNA-clamping. The present DNA sequence represents a PNA oligomer of the invention.
                                         /note= "This sequence is a peptide nucleic acid, (i.e. contains a polyamide backbone instead of a deoxyribose backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New peptide nucleic acid oligomer, useful as antisense molecules to treat bacterial and viral infections, has single units comprising different amino acid backbones such as aminoethylglycine -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·
0
                                                                                                                            /*tag= b
/mod_base= OTHER
/note= "The base is modified with Lys-NH2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 7; DB 24; L 100.0%; Pred. No. 5.7e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 7; Page 34; 40pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid microarray probe #3.
                       base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABK99556 standard; DNA; 10 BP
                                                                                                                                                                                                                                                                                                                                                    24-NOV-2000; 2000DK-0001776.
06-MAR-2001; 2001DK-0000371.
16-JUL-2001; 2001DK-0001117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-JUL-2001; 2001US-0899381
                                                                                                                                                                                                                                                                                                           23-NOV-2001; 2001WO-DK00779.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nielsen PE, Pueschl A;
                                                                                                                                                                                                                                                                                                                                                                                                                                              (PANT-) PANTHECO AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-490198/52.
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es 7; Conser
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                                                                                                                                                                                                                      WO200242316-A2
                                                                                                         modified_base
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                                                                                                                                                                                                                                                                 30-MAY-2002
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Synthetic

**ABK99556** 

RESULT 14 **ABK99556** 

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Gaps

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Novel isolated human Phospholipase A2, Group IB pancreas polynucleotide, for therapeutic purposes, for studying expression and function of the polynucleotide and for expressing the phospholipase protein 

The invention relates to an isolated human Phospholipase A2, Group IB Charactals (PLAZGIB) polymuclectide comprising a sequence which is a polymorphic variant for a reference sequence for the PLAZGIB gene or its fragment, or a polymorphic variant of a reference sequence for a reference sequence for a reference sequence for a pLAZGIB CDNA or its fragment. Also included are haplotyping/genotyping the haplotype pair for the PLAZGIB gene of an individual, identifying an association between a trait and at least one haplotype or haplotype pair of the PLAZGIB gene, an individual, identifying an association between a trait sequence, an individual placed detecting a polymorphism in the PLAZGIB gene, a recombinant non-human organism expresses a PLAZGIB computer sequence, where the organism expresses a PLAZGIB computer sequence or by the polymorphic variant of a reference sequence or by the polymorphic variant of a reference sequence for the PLAZGIB protein or test fragment, an anti-PLAZGIB monoclonal antibody, screening for drugs targeting PLAZGIB variant is sequence system for storing and analysing polymorphism data for the PLAZGIB gene and a genome anthology for PLAZGIB gene. The PLAZGIB variant is useful in studying the expression and for the pLAZGIB protein or functions of the pLAZGIB variant is studying the expression and founced the plazgible protein or for the pLAZGIB variant is studying the expression and founced the plazgible variant is successed to the plazgible variant is the plazgible variant is successed to the plazgible variant is successed to the plazgible variant is successed to the plazgible variant is the plazgible variant is successed to the plazgible variant is successed to the plazgible variant is the plazgible variant in the plazgible variant is the plazgible variant in the plazgible variant is the plazgible variant in the plazgible variant is the plazgible variant of the plazgible variant of the plaz efficacy of therapeutic agents and compounds in a biological system. The antibody is useful for studying the effect of the variation on the biological activity of PLA2G1B as well as on the binding affinity of candidate drugs targeting PLA2G1B. The PLA2G1B gene is located on chromosome 12g2-g24.1. The present sequence is an allele specific oligonucleotide (ASO) primer extension primer 3' end used to detect the function of PLA2CIB, and in expressing PLA2CIB protein for use in screening for candidate drugs to treat diseases related to PLA2CIB activity (e.g. pancreatitis and pancreatic cancer) and for therapeutic purposes. The transgenic organism is useful for studying expression of the PLA2CIB isogenes in vivo, for in vivo screening and testing of drugs targeted against PLA2CIB protein, and for testing the Claim 19; Page 13; 51pp; English polymorphisms in PLA2G1B

Sequence 10 BP; 3 A; 3 C; 0 G; 4 T; 0 other;

Gaps ö 100.0%; Score 7; DB 24; Length 10; 100.0%; Pred. No. 5.7e+04; 0; Indels 0; Mismatches O Query Match 100.
Off Best Local Similarity 100.
Matches 7; Conservative 1 AGTATGA 7

Cearch completed: December 31, 2003, 15:08:13

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ALIGNMENTS
                   H96935
AZ605844
AZ805844
AZ805844
AZ805846
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BH85761
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CZ1099
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AZ346766
AZ383946
               AZ816657
AZ817238
                                                                                                                                                                                                                                                                              ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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DEFINITION
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AZ817238
; Search time 804.291 Seconds (without alignments)
211.530 Million cell updates/sec
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   GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                 Gapop 10.0, vapen....

Searched: 22781392 seqs, 12152238056 residues

Ontain number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 30

Oper-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries
                                   December 31, 2003, 13:58:09
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                                                                              IDENTITY NUC Gapop 10.0 , Gapext 1.0
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AZ57956 1M0613016
AZ57956 1M06131113

Mus musculus (house mouse)

Kukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalla; Butheria; Rodentia; Sciurognathi; Muridae; Musn.

1 (bases 1 to 19)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil, C.,

Sobun,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.,
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah
Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5006
Fax: 801 585 7177 AZ817238 linear GSS 20-FEB-2001 2M0086E01R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0086E01 R, genomic survey sequence. AZ817238.1 GI:12987146 GSS. REFERENCE AUTHORS JOURNAL TITLE

> Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES

em\_gss\_phg:\* em\_gss\_vrl:\* gb\_gssl:\* gb\_gss2:\*

AZ817238 2M0086E01 AZ990856 2M0274F14 AZ623945 1M0462J10 AZ658158 1M0534H17 Description AZ817238 AZ990856 AZ623945 AZ658158 ΩI 28 28 28 28 28 DB Length 222 13 Query Match 100.0 100.0 100.0 Score ----4 2 C 4 Result Š. υυ

COMMENT

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoreals. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into adaptored vector DNA, and transformed into adaptored vector DNA, and transformed into chemically-competent E. Coli Killo-Gold (Stratagene) cells
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University of Utah Genome Center
University of Utah
Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSS 13-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AZ621945
1M0462J10F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0462J10 F, genomic survey sequence.
AZ623945
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Mus musculus
Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 22)
Munn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Menen, B., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
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100.0%; Pred. No. 2.1e+05;
ive 0, Mismatches 0;
                                Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0274 row: F column: 14
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                     organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                      db xref="taxon:10090"
                                                                                                                                                                                                                High quality sequence stop: 19.
                                                                                                                                                                                                                                                 Location/Qualifiers
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18 AGTATGA 12
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SOURCE
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
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2M0274F14R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus CS7BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

1 (bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longarcre, S., Mahmoud, M., Meenen, E., Pedersen, T., Resilly,

M., Rose, M., Stokes, R.,

and Wright, D., Weiss, R.,

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
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100.0%; Pred. No. 2.1e+05;
cive 0; Mismatches 0; Indels
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0086 row: E column: 01
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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organism="Mus musculus"
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University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                  db_xref="taxon:10090"
clone="UUGC2M0086E01"
                                                                                                                                                                            High quality sequence stop: 19.
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwalp4 (gil-#173114|gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coli XIIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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1 (bases 1 to 24)
Brenner,S., Williams,S.R., Vermass,E.H., Storck,T., Moon,K., McCollum,C., Mao,J.I., Kirchner,J.J., Bletr,S., DuBridge,R.B., Burcham,T. and Albrecht,G.
In vitro cloning of complex mixtures of DNA on microbeads: Physical separation of differentially expressed cDNAs
Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)
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AHuTH.bsst.dnc15.aa.A050g08 DNC15 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="B. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone_lib="Mouse_lokb_plasmid UNGCNM library"
/note="Wector: PWD47ny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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LYNX Therapeutics, Inc.
25861 Industrial Blvd., Hayward, CA 94545, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 7; DB 28; 100.0%; Pred. No. 2.2e+05;
                                                                         Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0534 row: H column: 17
Seq primer: CACACAGGAAACAGCTATGACC
Class: pleamid ends
High quality sequence stop: 22.
Location/Qualifiers
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                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                              /clone="UUGC1M0534H17"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                              'db_xref="taxon:10090"
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Best Local Similarity 100.v
                              Tel: 801 585 5606
Fax: 801 585 7177
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Walse, R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                /clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@enetics.utah.edu

Insert Length: 10000 Std Brror: 0.00

Plate: 0462 row: J column: 10
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                                                                                             Plate: 0462 row: J column: 10
Seg primer: CGTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
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University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0462J10"
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                                                                                                                                                                                                                                                                                                                                                                     /sex="Male
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1M0203P19F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0203P19 F, genomic survey sequence.
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84112, USA
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                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="DNC15"
//note="Vector: pCR2.1; Cloning of PCR products from micro-beads carrying 3' end of down-regulated cDNA. THP-1 cells non-induced (treated with DNSO only)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)
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Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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                                            Faai: timbolynxgen.com
Sequence obtained from LYNX Therapeutics Megasort technology.
Collected from the down-regulated gate.
High quality sequence stop: 24.

Location/Qualifiers
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                                                                                                                                                                                                                                                                 /mol type="mRNA"
/db xref="taxon:9606"
/cell type="monocyctic leukemia"
/cell line="THP-1" (TIB-202)"
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100.0%; Pred. No. 2.3e+05;
ive 0; Mismatches 0;
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insert Length: 10000 Std Error: 0.00
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Seq primer: CGTTGTAAAACGACGGCCAGT
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/organism="Mus musculus"
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/organism="Homo sapiens"
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University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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/clone="UUGC1M0203P19"
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Fax: 801 585 7177
Tel: 510 670 9338
                               Fax: 510 670 9302
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pw/42 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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musculus C57BL/6J (male) was obtained from the Jackson
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                    Laboratory Mouse DNA Resource
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/clone="UUGC1M0298J20"
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Mus musculus
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19 AGTATGA 13
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                                                                                                                          (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt endrepaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114[gb]AF129072.1). a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC, UT
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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2M0085E05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0085E05 R, genomic survey sequence.
                                                   musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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/note="Vector: PWD42nv; Purified genomic DNA from M.
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100.0%; Pred. No. 2.3e+05;
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Insert Length: 10000 Std Error: 0.00
Plate: 0085 row: E column: 05
Seq primer: CACACAGGAAACAGCTATGACC
Class: plaemid ends
High quality sequence stop: 24.
Location/Qualifiers
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/strain="C57BL/6J"
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/clone="UUGC2M0085E05"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Fax: 801 585 7177
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Best Local Similarity
7; Conserv?
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8 AGTATGA 2
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalp4 (gil 4732114 [gb]AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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1 (bases 1 to 2)
1 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, P., Trevaskis, E., Waterston, The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  yu01d01.r1 Soares pineal gland N3HPG Homo sapiens cDNA clone
IMAGE:232513 5' similar to SP:\(\bar{8}\)36112 $36112 RETINOBLASTOMA-BINDING
PROTEIN - ;, mRNA sequence.
/clone_lib="Mouse 10kb plasmid UUGCIM library"
//note="Twetcor: PWTA2Inv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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High quality sequence stops: 1
Source: IMAGE Consortium, LINL
This clone is available royalty-free through LINL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
ITACC considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 1325 Std Error: 0.00
Seq primer: M13RP1
Location/Qualifiers
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 24;
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/mol_type="mRNA"
/db_xref="GDB:3862504"
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Homo sapiens
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Best Local Similarity 100.
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(http://www.jax.org/resources/documents/dnares/). The DNA
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/lab hose="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse l0kb plasmid UUGC1M library."
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Seg primer: CGTTGTAAAACGACGGCCAGT
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/strain="C57BL/63"
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/clone="UUGC2M0061122"
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AZ802490.1 GI:12954813
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Fax: 801 585 7177
Email: ddunn@genet
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Best Local Similarity
7; Conserve
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                         AZ605844 13-DEC-2000 1M0427J22F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0427J22 F, genomic survey sequence.
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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/clone_lib="Mouse_lokb plasmid UTGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Insert Length: 10000 Std Error: 0.00
Plate: 0427 row: J column: 22
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers
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/mol type="genomic DNA"
/strain="C57BL/60"
/db xref="taxon:10090"
/clone="UUGC1M0427J22"
db xref="taxon:9606"
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Fax: 801 585 7177
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was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified asize-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil 4732114 [9b] AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xii0-Gold (Stratagene) cells and selected for ampicillin resistance."
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University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mamalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 25)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.,
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished
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2M0061122F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0061122 F, genomic survey sequence.
0.005 inch orifice at constant velocity. The sheared DNA
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100.0%; Pred. No. 2.3e+05;
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Insert Length: 10000 Std Brror: 0.00
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Gaps

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13-JUN-2002

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Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnollophyta, endicotyledons, core eudicots, rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.

(Dasse I to 2)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J. R.
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/clone='Ib='Arabidopsis thaliana TDNA insertion lines"
/clone='Ib='Arabidopsis thaliana TDNA insertion lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
the contains one or more the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
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SALK 075697.38.25.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_075697.38.25.x, genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
                                                                                                                Length 25;
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/mol_type="genomic DNA"
/strain="Columbia 0"
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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwd2 (gil #7732114 [gb] AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
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/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
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Contact: Joseph R. Ecker
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
The Salk Institute for Analysis Laboratory
The Salk Institute for Biological Studies
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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/strain="Columbia_0"
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(Dases 1 to 25)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
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/clone="SALK 015664.41.95.x"
/clone="SALK 015664.41.95.x"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, A., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse, Whole genome scaffolding with paired end reads from 10kb
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1M0080C06R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC1M0080C06 R, genomic survey sequence.
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Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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/mol_type="genomic DNA"
/strain="Columbia 0"
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                                                            BH857761.1 GI:21708582
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AZ345685.1 GI:10424922
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwapto (gilly 1712114 [gpl | AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coll XII0-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                        Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"/clone_lib="Mouse 10kb plasmid UUGCIM library"/note="Vector: PWD42nv; Purified genomic DNA from M.
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llarity 100.0%; Pred. No. 2.4e+05;
Conservative 0; Mismatches 0;
                                                                                                             Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: C column: 06
Seq primer: CACACAGGAAAACAGCTAATGACC
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/organism="Mus musculus"
University of Utah Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0080C06"
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Grotal number of hits satisfying chosen parameters:

Grinimum DB seq length: 0

Maximum DB seq length: 30

Maximum Match 0*

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Listing first 45 summaries
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Mcivor, R.S., Hackett, P.B. and Aguilar-Cordova, B.
Wector-mediated delivery of integrating transposon sequences
Vector-mediated delivery of integrating transposon sequences
Patent: WO 0068399-A 6 16-NOV-2000;
PREGENTS OF THE UNIVERSITY OF MINNESOTA (US); BAYLOR COLLEGE OF
MEDICINE (US); McIvor, R. Scott (US); Hackett, Perry B. (US);
Aguilar-Cordova, Estuardo (US)
Location/Qualifiers
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                                              Length 7;
                                              100.0%; Score 5; DB 6; Lv 100.0%; Pred. No. 5.8e+09;
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Corganism="synthetic construct"
/mol type="genomic DNA"
/db_xref="taxon:32630"

    .8
    /organism="synthetic construct"

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/db_xref="taxon:32630"
/note="birect Repeat Sequence"
3 c 0 g l t
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                                                                                            0; Mismatches
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Synthetic DNA Fragment"
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/organism="synthetic construct"
/mol type="genomic DNA"
/db xref="taxon:32630"
/note="Synthetic DNA Fragment"
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100.0%; Pred. No. 8.2e+09;
cive 0; Mismatches 0;
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db xref="texon.32630"
/noTe="Synthetic DNA Fragment"
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Axquence 3 from Patent W00174342.
AX268755 GI:16541827
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; MOLECULE TYPE: US-08-335-565A-27
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Patent No. 5532129
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Best Local (
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INFORMATION FOR SEQ ID NO:
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LENGTH: 10 base pairs
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0.
FILING DATE: 07-NOV-1991
                                                                                             COMPUTER READABLE FORM:
MBDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960
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MEDIUM TYPE: Floppy disk
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CLASSIFICATION: 435
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                                                                APPLICATION NUMBER: FILING DATE:
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1 South Pinckney St.,
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12526 High Bluff Drive, Suite 300
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SELF-CREANIZING MOLECULAR PHOTONIC
STRUCTURES BASED ON CHROMOPHORE- AND FLUF
POLYNUCLEOTIDES AND METHODS OF THEIR USE
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                         TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                               REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPHAX: (213) 955-0440
                                                                                                                                                                             FILING DATE: May 4, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/790,262
FILING DATE: No. 5565322ember 7, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                 SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Fitting, Thomas
REGISTRATION NUMBER: 34.
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Com
OPERATING SYSTEM:
                                                                                                                                               NAME: .Murphy, David B
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH:
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5; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       611 West Sixth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                IBM Compatible
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T nucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRUCTURES BASED ON CHROMOPHORE- AND FLUOROPHORE-CONTAINING POLYNUCLEOTIDES AND METHODS OF THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SELF-ORGANIZING MOLECULAR PHOTONIC
STRUCTURES BASED ON CHROMOPHORE- AND FLUOROPHORE-
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Pred. No.
                                                                                                                                                                                                                                                                                                                                     (Version 5.0)
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8.6e+04;
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RESULT 14

Matches

0

Gaps

Sequence 80,

Application

US/08646789A

No.

GENERAL INFORMATION:

APPLICANT: Peyman, John A.
TITLE OF INVENTION: REGULATION OF GENE EXPRESSION

Matches Query Match Best Local

Similarity
5; Conserv

Conservative

0

Mismatches

0

Gaps

0

100.0%;

Score 5; Pred. No.

DB 3; L

Length 9; Indels

101

CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES:

DDRESSEE:

1155 Avenue of the Americas

PENNIE & EDMONDS

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Length 9;
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Best Local Similarity
Thes 5; Conserv
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                                                                                    US-08-335-565A-27
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                                                                                                     RESULT 13
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                                               Patent No. 552767
                                                                    Sequence 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 68, Applicati
Patent No. 6451530
GENERAL INFORMATION:
               GENERAL INFORMATION:
APPLICANT: Li, Kening
                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,844
FILING DATE: 13-DEC-1996
APPLICATION NUMBER: WO PCT/US97/22448
FILING DATE: 10-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/319,648
FILING DATE: 30-Uul-1999
CLASSIFICATION: -Unknown>
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESONDENCE ADDRESS:
CORRESONDENCE: Townsend and Townsend and Crew LLP
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID NO: 68:
                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hawkins, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GTATG 5
                                                                                                                                                                                    1 GTATG 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Fang, Carol REGISTRATION NUMBER: 48,631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTATG
                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 015280-288100US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX:
                                                                    Application US/08335565A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/09319648
Rouse, Douglas I.
                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                           linear
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Fluorescent Nucleotide Analog Hairpin
Formation for Detection of Nucleic Acid Hybridization
                                                                                                                                                                                                                                                                                                                                                                                                                                           576-0300
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Pred. No.
                                                                                                                                                                                                                         Mismatches
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4.5e+07,
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밁 S

Sequence 1, Application US/09048927 Patent No. 6147056

INFORMATION:

APPLICANT: Gilchrest, Barbara A. APPLICANT: Yaar, Mina APPLICANT: Eller, Mark

SEQ ID NO 1

LENGTH: 9

NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0

TITLE OF INVENTION: Use of Locally Applied DNA Fragments FILE REFERENCE: BU94-68A2
CURRENT APPLICATION NUMBER: US/09/048,927
CURRENT FILING DATE: 1998-03-26
EARLIER APPLICATION NUMBER: 08/952,697
EARLIER FILING DATE: 1996-06-03
EARLIER APPLICATION NUMBER: 08/467,012
EARLIER FILING DATE: 1995-06-06

OTHER INFORMATION: DNA Fragment 09-048-927-1

TYPE: DNA
ORGANISM: Artificial Sequence

FEATURE:

US-08-646-789A-80

STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: RNA

TYPE: nucleic acid

ENGTH:

9 base pairs

ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6523-(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864

6523-006

CLASSIFICATION:

APPLICATION NUMBER: US/08, FILING DATE: May 21, 1996

SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:

US/08/646,789A

COMPUTER READABLE FORM:

10036-2711

STATE: New York COUNTRY: U.S.A. CITY: New York

MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

INFORMATION FOR SEQ ID NO:

66141

PENNIE

SEQUENCE CHARACTERISTICS:

Best Local Similarity
Matches 3; Conserv.

Conservative

100.0%; Score 5; DB 3; 60.0%; Pred. No. 4.5e+07; tive 2; Mismatches 0

Query Match

Copied from 09980559 on 05/19/

0

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US-08-583-276-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PILING DATE: 11-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/053
PILING DATE: 28-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/065
PILING DATE: 13-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US
PILING DATE: 11-MAR-1998
APPLICATION NUMBER: US/08/583,2
FILING DATE: 05-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/332,444
FILING DATE: 31-OCT-1994
                                                                                        COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DC
SOFTWARE: DW4.V2
CURRENT APPLICATION DATA:
                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                     ADDRESSEE: Carella, Byrne, Bain, Gilfillan, STREET: 6 Becker Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: SANDBERG, VICTORIA A. REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 111
                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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5837536
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                                                                                                                                                                                                                               F: 6 Becker Farm Road
Roseland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
EDNESS: single
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                                                                                                                                                                                                                 New Jersey
                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                 Nienhuis, Arthur
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                                                                                                                                                                                                                                                                                                                                                                                               McDonagh, Kevin T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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MULTIDRUG RESISTANCE GENES AND IMPROVED
SELECTION OF CELLS TRANSDUCED WITH SUCH GENES
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                                                                             US/08/583,276
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Pred. No.
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US-08-646-789A-80
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US-08-646-789A-8
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                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                      TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION: APPLICANT: Peyman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 22-MAY-1
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-L
SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                 TOPOLOGY: 1:
                                                                                                                                                                                                                                                                                                                     NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,972
REFERENCE/DOCKET NUMBER: 652:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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nes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: singular
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                    TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: May CLASSIFICATION: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: New York
                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                           TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/646,789A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
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                                                                                                                                       Local
                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DESCRIPTION: Genomic DNA
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                                                                                                                         Similarity 5; Conserv
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                                                                                            GTATG 5
                                                              GTATG 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New York
                                                                                                                                                                                                                                                           9 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1155 Avenue of the Americas
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                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peyman, John A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PENNIE & EDMONDS
                                                                                                                                                                                                  DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-MAY-1992
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                                                                                                                                       Score 5;
Pred. No.
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Pred. No.
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                                                                                                                                        4.5e+07;
                                                                                                                                                     Length 9;
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Matches

Patent No.

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RESULT 5
US-08-615-170-12/c
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Best Local
                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 04-FEB-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 326-2400
                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNBER: PCT/US95/01526
FILING DATE: 06-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                              SOPTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                     NAME: Heslin, James M.
REGISTRATION NUMBER: 29
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: /standard_name= "Sph-II binding OTHER INFORMATION: site in SV40"
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                      STRANDEDNESS:
                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                  ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T: STEWART, Alexand T: LARKIN, Sarah B. INVENTION: DTEF-1
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                                                    7 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Steuart Street Tower,
                                                                                                     (415) 326-2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AZAKIE, Anthony
MAR, Janet H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FARRANCE, Iain K.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Townsend and Townsend Khourie and Crew euart Street Tower, One Market Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Deborah E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Charles P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DTEF-1 ISOFORMS AND USES THEREOF
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Pred. No.
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                                                                                                                                                                                                                                                                                                                        RESULT 7
US-09-142-593-11/c
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Best Local Similarity
Tatches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: DNA Fragment US-09-048-927-3
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                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                        Sequence 11, Application US/09142593
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Best Local Similarity
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Patent No. 614705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EARLIER FILING DATE: 1996-06-03
EARLIER APPLICATION NUMBER: 08/467,012
EARLIER FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 4
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/048,927
CURRENT FILING DATE: 1998-03-26
EARLIER APPLICATION NUMBER: 08/952,697
EARLIER FILING DATE: 1996-06-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gilchrest, I
APPLICANT: Yaar, Mina
APPLICANT: Eller, Mark
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                 TITLE OF INVENTION: DN:
TITLE OF INVENTION: INV
NUMBER OF SEQUENCES: 6:
CORRESPONDENCE ADDRESS:
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FEATURE:
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OTHER INFORMATION:
OTHER INFORMATION:
                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                   COUNTRY:
                                                                                                                                                   STREET:
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IT: 119 NORTH FOURTH STREET, SUITE 203
MINNEAPOLIS
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PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                      DNA-BASED TRANSPOSON SYSTEM FOR THE INTRODUCTION OF NUCLEIC ACID INTO DNA OF A CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 5;
100.0%; Pred. No.
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Heavy Chain M-CAT binding element"
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Pred. No.
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5.8e+07;
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5.8e+07;
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US-09-498-851-20
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20, Application US/09498851
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CURRENT FILING DATE: 1998-03-26
EARLIER APPLICATION NUMBER: 08/952,697
EARLIER FILING DATE: 1996-06-03
EARLIER APPLICATION NUMBER: 08/467,012
EARLIER FILING DATE: 1995-06-06
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APPLICANT: Yaar, Mina
APPLICANT: Eller, Mar]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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OTHER INFORMATION: DNA Fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tent No.
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH:
                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/855,372
FILING DATE: 13-MAY-97
                                                                                                   COMPUTER: PC
OPERATING SYSTEM: Microsoft Windows 98
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: 3.50 in
                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHERSKOV & FLAYNIK
                                                                                                                                                                                                                                                                                                                                            APPLICANT: Dubiley, Svetlana A
IITLE OF INVENTION: Use of Continuous/Contiguous
IITLE OF INVENTION: Stacking Hybridization as a Diagnostic Tool
                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                  APPLICATION NUMBER: FILING DATE:
APPLICATION NUMBER: U.S. 08/587,332
                                                                                                                                                                                                                            COUNTRY:
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                                                                                                                                                                                                                                              Illinois
                                                                                                                                                                                                                            United States
                                                                                                                                                                                                                                                                           20 N. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                    Parinov, Sergei
Barsky, Victor E
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mirzabekov, Andrei D
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                                                                                                                                                                                                                                                                                                                                                                                                  Kirillov, Eugene V
                                                                                                                                                                      3.50 inch, 1.4 MB storage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
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                                                                                      US/09/498,851
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Pred. No. 8.2e+07;
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INFORMATION FOR SEQ ID NO: 20:
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MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tent No.
                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/615,170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/191,493
                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/I
FILING DATE: 06-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Computible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (312) 621-1330
                                                                                                                 FILING DATE: 04-FEB-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: LARKIN, TITLE OF INVENTION:
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                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Cherskov, Michael
REGISTRATION NUMBER: 33
REFERENCE/DOCKET NUMBER:
                                                                  NAME: Heslin, James M. REGISTRATION NUMBER: 29 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: No. 6440671 Applicable
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                  TELEPHONE:
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ilarity 100.0%;
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                (415) 326-2400
(15) 326-2422
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Pred. No.
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Total number of hits satisfying chosen parameters:
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
6: /cgn2_6/ptodata/1,
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Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
Listing first 45 summaries
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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113.581 Million cell updates/sec
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                                         US-08-855-372B-20
US-09-498-851-20
US-09-498-851-20
US-09-498-851-70-12
US-08-615-170-12
US-08-615-170-12
US-08-646-789A-8
US-08-646-789A-8
US-08-646-789A-8
US-08-646-789A-8
US-08-351-565A-27
US-08-250-951-1
US-08-222-177A-22
US-08-351-748-25
                         S-08-351-748-23

S-08-351-748-25

S-08-202-2927-25

S-08-430-536A-23

S-08-430-536A-25

S-08-171-718-45

S-08-703-601-1

S-08-684-547-25

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Sequence 20, Appl
Sequence 4, Appli
Sequence 10, Appl
Sequence 10, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 27, Appli
Sequence 1, Appli
Sequence 27, Appli
Sequence 23, Appli
Sequence 23, Appli
Sequence 25, Appl
Sequence 27, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                             ; TYPE: nucleic acid
; STRANDENNESS: No. 6090549;
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: yes
US-08-855-372B-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1
US-08-855-372B-20
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                         Query Match
Best Local :
     Matches
                                                                                                                                                                                                                                      TELEFAX: (312) 621-0088 INFORMATION FOR SEQ ID NO: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 20 N. Wacker Drive
CITY: Chicago
STATE: Ilinois
COUNTRY: United States
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.50 inch, 1.4 MB storage
                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/855,372B
FILING DATE: 13-MAY-97
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/587,332
FILING DATE: 16-JAN-96
ATTORNEY/AGENT INFORMATION:
NAME: Cherskov, Michael J.
                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 33,664
REFERENCE/DOCKET NUMBER: ANL-IN-95-027
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 621-1330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: PC
OPERATING SYSTEM: Microsoft Windows 98
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHERSKOV & FLAYNIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Use of Continuous/Contiguous Stacking Hybridization as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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   l Similarity
5; Conserv
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Barsky, Victor E
Kirillov, Eugene V
Dubiley, Svetlana A
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Parinov, Sergei V
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US-09-063-450-24
US-09-063-450-33
US-09-123-638-1
US-08-646-695-30
US-08-646-695-31
US-08-724-753-1
US-08-762-227A-174
US-09-475-947A-23
US-09-427-834A-34
US-09-445-38B-25
US-09-485-38B-25
US-09-508-753B-26
US-09-508-753B-273
US-09-508-753B-273
US-09-508-753B-273
US-09-508-753B-273
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   Score 5; DB
Pred. No. 8.2
D; Mismatches
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8.2e+07;
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174, App
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252, Appl
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273, Appl
274, Appl
275, Appl
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278, Appl
279, Appl
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Result No.

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Post-processing:

Minimum DB seq length: Maximum DB seq length:

Scoring table: Sequence: Perfect score:

OM nucleic -

Copyright

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December 31,

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APPLICANT: Reinhard, Christoph
APPLICANT: Jefferson, Anne B.
APPLICANT: Winter, Jill A.
APPLICANT: Winter, Jill A.
APPLICANT: Randazzo, Filippo
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: NEOPLASTIC DISEASE USING NET-4 MODULATORS
FILE REFERENCE: PP-01701.002/200130.522
CURRENT APPLICATION NUMBER: US/09/875,440
CURRENT FILING DATE: 2001-06-05
NUMBER OF SEQ ID NOS: 22
SOFTWARR: FastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 14
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide NET-4 oligo 868 used for in-situ
OTHER INFORMATION: hybridization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REFERENCE: MUBHB00.9601-F
CURRENT APPLICATION NUMBER: US/09/817,879
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE: PAtentin version 3.0
SEQ ID NO 4624
LENGTH: 13
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc_feature
LOCATION:
OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-4624
Search completed: January 1, 2004, 01:10:36 Job time : 82.6076 secs
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Best Local Similarity 71.*
Thes 5; Conservative
                                                                                                                                                                Query Match 100.0%; Score 7; Best Local Similarity 100.0%; Pred. No. Matches 7; Conservative 0; Mismatch
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6 AGUAUGA 12
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hes 0;
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RESULT 10 US-10-033-145-1423/c

GENERAL INFORMATION:

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APPLICANT: GENZYME CORPORATION
APPLICANT: ROBERTS, BRICE
APPLICANT: SHANKARA, SRINIVAS
APPLICANT: SHANKARA, SRINIVAS
TITLE OF INVENTION: PREPARATION AND USE OF SU
FILE REFERENCE: GA0201C
CURRENT APPLICATION NUMBER: US/10/033,145
CURRENT FILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: PCT/US99/13800
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 2137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1423, Application US/10033145 Publication No. US20020151515A1
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                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: ORUM, HENRICK
APPLICANT: HANSEN, BO
TITLE OF INVENTION: THERAPEUTIC USES OF INA-MODIFIED OLIGONUCLEOTIDES
TITLE OF INVENTION: INFECTIOUS DISEASES
TITLE OF INVENTION: INFECTIOUS DISEASES
TITLE OF INVENTION: INFECTIOUS DISEASES
TITLE OF INVENTION: UNDEER: US/10/150,779A
CURRENT APPLICATION NUMBER: US/10/201,830
PRIOR APPLICATION UMBER: 60/291,830
PRIOR FILING DATE: 2001-05-18
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: oligonucloetide
                                                                                                                                             100.0%; Score 7;
100.0%; Pred. No.
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Pred. No. 1.1
0; Mismatches
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RESULT 14
US-09-817-879-4624
; Sequence 4624, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                     ; PEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-4624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-740-332-4624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases
TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REFERENCE: RPI 400/003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: HANSÉN, BO
TITLE OF INVENTION: THERAPEUTIC USES OF LNA-MODIFIED OLIGONUCLEOTIDES
TITLE OF INVENTION: THERCITIOUS DISEASES
FILE REFERENCE: 55704 (45120)
CURRENT FILING LOTE: 2003-02-07
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: 60/291,830
PRIOR APPLICATION NUMBER: 60/291,830
PRIOR FILING DATE: 2001-05-18
NUMBER OF SEQ ID NOS: 16
SOPTWARE: PATENTIN VEY: 2.1
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/740,332
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9704
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4624
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                                                                                                                                                                                                                           Matches
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Best Local
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Best Local
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 13
TYPE: RNA
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                                                                                                                                                                                                                         . Similarity 5; Conserv
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ORUM, HENRICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Pred. No.
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Pred. No. 1.1e+05
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1.1e+05;
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US-10-150-779A-15/c

GENERAL INFORMATION:

APPLICANT: WISSENBACH, MARGIT APPLICANT: KOCH, TROELS

KOCH, TROELS ORUM, HENRICK

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US-10-150-779A-15

Query Match Best Local (

Local Similarity

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Matches

SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 12
TYPE: DNA

; ORGANISM: Homo sapiens US-10-033-145-1423

SOFTWARE: PatentIn version 3.0 SEQ ID NO 1423

ENGTH: 10

ORGANISM: Artificial FEATURE:

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RESULT 7
US-09-398-399-31
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US-10-122-633-1
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                                                                                                                                                                                       APPLICANT: DELENSTARR, GLENDA C.
APPLICANT: LEFKCWITZ, STEVEN M.
APPLICANT: LUEBKE, KEVIN J
APPLICANT: OVERMAN, LESLIE B.
APPLICANT: SAMPRAS, NICHOLAS M.
APPLICANT: SAMPRAS, NICHOLAS R.
APPLICANT: WOLBER, PAUL K.
                                                                                                                                                                                                                                                                                                                          Sequence 31, App...
No. US2002
                      SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 31
LENGTH: 10
TYPE: DNA
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Best Local Similarity
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APPLICANT: Gilchrest,
APPLICANT: Bller, Man
APPLICANT: Yaar, Mina
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Best Local Similarity
                                                                                    CURRENT APPLICATION NUMBER: US/09/398,399
CURRENT FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 35
                                                                                                                                       TITLE OF INVENTION: TECHNIQUES FOR ASSESSING NONSPECIFIC BINDING TITLE OF INVENTION: ACIDS TO SURFACES FILE REFERENCE: 10981620-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/122,633
CURRENT FILING DATE: 2002-04-12
CURRENT PILING UNMBER: US 09/540,843
PRIOR APPLICATION NUMBER: US 09/540,843
PRIOR FILING DATE: 2000-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Method to Inhibit Cell Growth Using TITLE OF INVENTION: Oligonucleotides FILE REFERENCE: 0054.1088-019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Synthetic DNA Fragment
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     ORGANISM: Artificial Sequence
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Pred. No.
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Best Local Similarity
"hes 7; Conservations
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                                                                    ; OTHER INFORMATION: US-10-329-465-30
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                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/343,826
PRIOR FILING DATE: 2001-12-27
NUMBER OF SEQ ID NOS: 315
SOFTWARE: Patentin version 3.1
SEQ ID NO 30
               Query Match
Best Local
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 31
LENGTH: 10
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   Matches
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                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/329,465
CURRENT FILING DATE: 2002-12-23
                                                                                                                                                                                                                                                                                          APPLICANT: Wang et al.
TITLE OF INVENTION: GENES ABNORMALLY EXPRESSED TITLE OF INVENTION: FUSION
FILE REFERENCE: 27373/37928A
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CURRENT FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 09/398,399
PRIOR FILING DATE: 1999-09-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Arrays Having Background Features
                                                                                                             TYPE: DNA
ORGANISM: Artificial sequence
                                                                                                      FEATURE:
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OTHER INFORMATION: synthetic probe
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PRIOR FILING DATE: 1995-06-06
PRIOR PELICATION NUMBER: PCT/US96/08386
PRIOR FILING DATE: 1996-06-03
PRIOR APPLICATION NUMBER: US 09/048,927
PRIOR APPLICATION NUMBER: US 09/540,843
PRIOR APPLICATION NUMBER: US 09/540,843
PRIOR APPLICATION NUMBER: US 09/540,843
PRIOR APPLICATION NUMBER: PCT/US01/10162
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Publication No. US20030032611A1
GENERAL INFORMATION:
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Best Local
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                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 3
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                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Method to Inhibit Cell Growth Using TITLE OF INVENTION: Oligonucleotides FILE REFERENCE: 0054.1088-019
CURRENT APPLICATION NUMBER: US/10/122,633
CURRENT FILING DATE: 2002-04-12
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CURRENT APPLICATION NUMBER: US/10/122,630
CURRENT FILING DATE: 2002-04-12
                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: PCT/US01/10162 PRIOR FILING DATE: 2001-03-30
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APPLICANT: Eller, Mark S.
APPLICANT: Yaar, Mina
                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 09/540,843 PRIOR FILING DATE: 2000-03-31
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                       OTHER INFORMATION: Synthetic DNA Fragment
                                                               TYPE: DNA
ORGANISM: Artificial Sequence
                                              FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 7; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                        Eller, Mark S.
Yaar, Mina
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                                                                                                                                PRIOR APPLICATION NUMBER: US 08/467,012
PRIOR FILING DATE: 1995-06-06
PRIOR PELICATION NUMBER: PCT/US96/08386
PRIOR FILING DATE: 1996-06-03
PRIOR APPLICATION NUMBER: US 09/048,927
PRIOR APPLICATION NUMBER: US 09/540,843
PRIOR APPLICATION NUMBER: US 09/540,843
PRIOR APPLICATION NUMBER: US 09/540,843
PRIOR PILING DATE: 2000-03-31
SEQ ID NO 1
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/10122630 Publication No. US20030032610A1
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                                                                                        PRIOR APPLICATION NUMBER: PCT, PRIOR FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/122,630 CURRENT FILING DATE: 2002-04-12
                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Method to Inhibit Cell Growth Using TITLE OF INVENTION: Oligonucleotides FILS REFERENCE: 0054.1088-018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gilchrest, APPLICANT: Eller, Mai APPLICANT: Yaar, Mina
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Gilchrest, Barbara A.
APPLICANT: Eller, Mark S.
APPLICANT: Yaar, Mina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Synthetic DNA Fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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7; Conser
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Yaar, Mina
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                                                                      ID NOS:
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Pred. No.
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Query Match
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Matches 7
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Publication No. US20030032611A1
                                                                                                               TITLE OF INVENTION: Method to Inhibit Cell Growth Using TITLE OF INVENTION: Oligonucleotides FILE REFERENCE: 0054.1088-019 CURRENT APPLICATION NUMBER: US/10/122,633 CURRENT FILING DATE: 2002-04-12
                  PRIOR APPLICATION NUMBER: US 09/540,843
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: PCT/US01/1016:
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                           PCT/US01/10162
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Pred. No.
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Mismatches

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Perfect score:
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.

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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*

13: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*

14: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

15: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

16: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/US10B_PUB.seq:*

17: /cgn2_6/ptodata/1/pubpna/US10B_PUB.seq:*

18: /cgn2_6/ptodata/1/pubpna/US10B_PUB.seq:*
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Match
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Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
Listing first 45 s
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          5 US-10-122-630-7

5 US-10-122-633-7

5 US-10-122-633-7

5 US-10-122-633-1

5 US-10-122-633-1

US-10-122-633-1

US-09-398-399-31

US-09-398-399-31

US-10-399-465-30

4 US-10-130-79A-15

5 US-10-150-779A-15

5 US-10-150-779A-15

5 US-10-150-779A-15

6 US-09-740-332-4624

3 US-09-740-332-4624
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Compugen Ltd
Sequence 3, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 1423, Appl
Sequence 15, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 4624, Ap
Sequence 4624, Ap
Sequence 4624, Ap
                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                      TITLE OF INVENTION: Oligonucleotides
FILE REFERENCE: 0054.1088-018
FILE REFERENCE: 0054.1088-018
CURRENT APPLICATION NUMBER: US/10/122,630
CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: US/867,012
PRIOR FILING DATE: 1995-06-06
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US/9/048,927
PRIOR APPLICATION NUMBER: US/9/048,927
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: US/9/540,843
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: US/9/540,843
PRIOR APPLICATION NUMBER: US/9/540,843
PRIOR APPLICATION NUMBER: US/9/540,843
PRIOR APPLICATION NUMBER: US/9/540,843
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 7
TYPE: DAN Artificial Commons
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                                                                                                                   ; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment US-10-122-630-3
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US-10-122-630-3
            Query Match
Best Local Similarity 100.
Thes 7; Conservative
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APPLICANT: Gilchrest, Barbara A.
APPLICANT: Eller, Mark S.
APPLICANT: Yaar, Mina
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                                                                                                                                                                          ORGANISM: Artificial Sequence
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100.0%; Pred. No.
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US-09-504-231A-528
US-09-504-231A-1529
US-09-504-231A-1527
US-09-504-231A-1570
US-09-504-231A-1570
US-09-38-399-30
US-09-38-399-30
US-09-274-553D-527
US-09-274-553D-1527
US-09-274-553D-1527
US-09-274-553D-1569
US-09-274-553D-1569
US-09-274-553D-1569
US-09-274-553D-1570
US-09-274-553D-1570
US-09-272-343-2
US-09-272-343-2
1 US-09-272-343-2
1 US-09-740-332-4558
US-09-740-332-4558
US-09-866-108-2750
US-09-866-108-2753
US-09-866-108-2756
US-09-866-108-2756
                                          0; Mismatches
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                                                          DB 15; 1
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                                        Indels
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US-08-182-968A-168/c
RESULT 15
US-08-182-968A-169/c
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Best Local S
Matches 8
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Patent No. 6096505
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                                                                                                                      Matches
                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/182,
FILING DATE: 13-JANUARY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/882,888
FILING DATE: 14-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (1)..(12) FEATURE:
                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                  TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Com
OPERATING SYSTEM:
                                                                                                                                                                                               STRANDEDNESS:
TOPOLOGY: li
                                                                                                                                                                                                                         TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                         NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A. ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: California
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Los Angeles
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8; Conserv
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                                                           AGGAGGAT 6
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VENTION: METHOD AND REAGENT FOR
VENTION: INHIBITING HEPATITIS C
                                                                                                                    Conservative
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linear
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                                                                                                                               88.9%; Score 8;
100.0%; Pred. No.
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                                                                                                                    Mismatches
                                                                                                                                DB 1; Leno. 1.3e+04;
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o. 1.2e+04;
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                                                                                                                                              Length 15
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Best Local Similarity
Warches 8; Conserve
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Conservative

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Score 8; DB 1; Pred. No. 1.3
0; Mismatches

DB 1; Le o. 1.3e+04;

Length 15, Indels

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Gaps

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US-08-182-968A-169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 5610054
GENERAL INFORMATION:
                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 15
                                                                                                                                                                              APPLICATION NUMBER: US/08/:
FILING DATE: 13-JANUARY-19!
PRIOR APPLICATION DATA:
APPLICATION UMBER: 07/882
FILING DATE: 14-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,32'
REFERENCE/DOCKET NUMBER: 20
                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C.
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Di
MEDIUM TYPE: storage
                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                  TELEFAX: (411.
             STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                             TELEPHONE:
                                         nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/08182968A
                                                                                                                                (213) 489-16
(213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Draper, Kenneth G.
VENTION: METHOD AND REAGENT FOR
VENTION: INHIBITING HEPATITIS C
               linear
                                                                                                                                                                                                                                                                                               13-JANUARY-1994
                             single
                                                                                                                                                   489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                 Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VIRUS REPLICATION
                                                                                                                                                                                                                                                                 07/882,888
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                                                                                                                                                                                            32,327
                                                                                                169:
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US-08-310-356-20
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                              CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07,
FILING DATE: 31-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Goodman, Rosanne
                                                                                     TELEFAX: (215) 454-3808
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 39,395
REPERENCE/DOCKET NUMBER: 1242/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 493-8000
TELEPAX: (919) 419-0383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: ARLES A. TAYLOR, J
                                                                                                                                                                                                                                                                                                   COMPUTER: Macintosh System 7.
OPERATING SYSTEM: Macintosh System 7.
SOFTWARE: Microsoft Word Version 5.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                               ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Transgenic Protein Production NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hurwitz,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA: NONE APPLICATION NUMBER:
                                                                                                                NAME: Goodman, Rosanne
REGISTRATION NUMBER: 32,534
REFERENCE/DOCKET NUMBER: A00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 454-3817
                                                                          SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                         LENGTH: 29 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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Similarity 100.0%;
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Shani, Moshe
                                                                                                                                                                                                                                                                                                                                                                                                               USA
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Pred. No.
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2.8e+03;
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US-09-019-793A-105/c
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Patent No.
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Best Local
                                                                          SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 15
                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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Best Local (
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APPLICANT:
APPLICANT:
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                                                                                                        NUMBER OF SEQ ID NOS: 20
                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                           ORGANISM: Artificial Sequence
                                                          ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23
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9; Conserv
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100.0%;

DB 4; Lo 2.9e+03;

Length 30

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; OTHER INFORMATION: Description of Artificial Sequence:synthetic US-09-019-793A-105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 105, Application US/09019793A
                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 08/478,316
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/301,435
PRIOR FILING DATE: 1994-09-01
PRIOR APPLICATION NUMBER: 08/131,625
PRIOR FILING DATE: 1993-10-05
PRIOR APPLICATION NUMBER: 07/969,071
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: MOROZOV, IGOR
APPLICANT: HALBUR, PARTICK
APPLICANT: HALBUR, PARTICK
TITLE OF INVENTION: PROTEINS ENCODED BY POLYNUCLEIC ACIDS OF PORCINE
TITLE OF INVENTION: REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS (PRRS
FILE REFERENCE: 4655-0039-55X CIP
CURRENT APPLICATION NUMBER: US/09/019,793A
CURRENT FILING DATE: 1998-02-06
                                                                                                                                                                                PRIOR FILING DATE: 1
NUMBER OF SEQ ID NOS:
                                                               LENGTH: 30
TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                               PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAUL, Prem
MENG, Xiang-Jin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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100.0%; Pred. No.
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2.8e+03;
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RESULT 6
US-09-416-050A-15/c
; Sequence 15, Application US/09416050A
; Patent NO. 6194559
. GENERAL INFORMATION:

*TM. Soo Young
                                                                                                                                                                                                                                                                       ; SEQ ID NO 15; LENGTH: 24; TYPE: DNA; TYPE: DNA; ORGANISM: Arabidopsis thaliana US-09-664-800-15
                                                                                                  US-09-665-309-15/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local
Matches
                                                       Sequence 15, Application US/09665309 Patent No. 6232461 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15, Application US/09664800 Patent No. 6218527
                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION: APPLICANT: KIM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 15
LENGTH: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Arabidopsis thaliana
-09-416-050A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: KIM. Soo Young
TITLE OF INVENTION: Absolsic Acid Responsi
FILE REFERENCE: 1942/42
CURRENT APPLICATION NUMBER: US/09/416,050A
CURRENT FILING DATE: 1999-10-12
 FILE REFERENCE: 1942/42
CURRENT APPLICATION NUMBER: US/09/665,309
                        APPLICANT: KIM. S
                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1999
                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/664,800 CURRENT FILING DATE: 2000-09-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ITLE OF INVENTION:
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                                          KIM. Soo Young
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                        Abscisic Acid Responsive Element -Binding Transcription Factor
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Pred. No. 2.8
0; Mismatches
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Pred. No.
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; ORGANISM: Arabidopsis thaliana
US-09-665-309-15
                                                                                                                                                                                                                                                                                                             US-09-061-768A-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Arabidopsis thaliana US-09-661-569-15
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Patent No. 6245.
PATERAL INFORMATION:
KIM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
SOFTWARE: FASTSEQ fo
SEQ ID NO 15
LENGTH: 24
                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                Sequence 33, Application US/09061768A
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Best Local (
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SEQ ID NO 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local
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CURRENT FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 09/416,050
PRIOR FILING DATE: 1999-10-12
                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
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PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.
COMPUTER: IBM PC/XT/AT compatible
OPERATING SYSTEM: Windows 3.1
SOFTWARE: WORD PERFECT 6.1 and ASCII
                                                                                                                                                                                                             APPLICANT: JISAKA, MITSUO
TITLE OF INVENTION: LIPOXYGENASE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH:
             CURRENT APPLICATION DATA
                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                       APPLICANT:
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Local Similarity 100.0%;
les 9; Conservative 0
 APPLICATION NUMBER:
                                                                                                  COUNTRY: U
                                                                                                                                                                    ADDRESSEE:
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9; Conserva
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NORTH CAROLINA
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                                                                                                                                                     SUITE 1400, UNIVERSITY
                                                                                                               USA
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1999-10-12
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US/09/061,768A
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Pred. No. 2.8
0; Mismatches
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Pred. No.
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                                                                                                                                                      TOWER,
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                                                                                                                                                        3100 TOWER BOULEVARD
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                                                                    storage
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US-09-422-978-6304/c
; Sequence 6304, Application US/09422978
; Patent No. 6537751
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Best Local
                                                                                                                           SEQ ID NO 6304
                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-11-23
                                                                                                                                                                                                                                                                                             APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CP1
                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cohen, Danier
APPLICANT: Blumenfeld, Mar
APPLICANT: Chumakov, Ilya
                                                                                                                                                            EARLIER FILING DATE: 1998-04-21
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                                                           TYPE: DNA
ORGANISM: Homo Sapiens
                  NAME/KEY: primer_bind LOCATION: 1..20
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HYPOTHETICAL: NO
TENSE: YES
                                                         FEATURE:
OTHER INFORMATION: upstream amplification primer 99-10661 for SEQ 2370
                                                                                                           LENGTH: 20
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PRIOR APPLICATION DATA:
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RELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
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FILING DATE: 04-JAN-1
APPLICATION NUMBER: F
FILING DATE: 04-JAN-1
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OPERATING SYSTEM: PC-DOS/MS-DOS
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NUMBER: US 60/109,732
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100.0%; Pred. No.
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                                    US-09-240-918-9
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US-09-240-918-9
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 Query Match
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                                                                                                                                                                                                                         APPLICANT: XU, Zhidong
TITLE OF INVENTION: METHODS FOR EST-SPECIFIC FULL LENGTH CDNA CLONING
FILE REFERENCE: 480.85.1(HV)
CURRENT APPLICATION NUMBER: US/09/240,918
CURRENT FILING DATE: 1999-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EARLIER APPLICATION NUMBER: US 09/298,850 EARLIER FILING DATE: 1999-04-21 EARLIER APPLICATION NUMBER: US 60/109,732 EARLIER FILING DATE: 1998-11-23 EARLIER APPLICATION NUMBER: US 60/082,614 EARLIER FILING DATE: 1998-04-21
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PRIOR FILING DATE: 1998-11-12
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CURRENT FILING DATE: 1999-10-20
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APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CP1
                                                                                                                                                                               NUMBER OF SEQ ID NOS: 96
                                                                                                                                                                                                                                                                                                     APPLICANT: Gruenert, Dieter C. APPLICANT: Xu, Zhidong
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo Sapiens
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                                                                                                         TYPE: DNA
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                                                                                      ORGANISM: Artificial Sequence
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                                                   Description of Artificial Sequence: primer
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100.0%; Pred. No.
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Pred. No.
 Score 9;
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2.8e+03
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Length 22;
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Maximum
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Match
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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          GenCore version (c) 1993 - 2004
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US-09-240-918-9
US-09-661-909-15
US-09-665-309-15
US-09-661-569-15
US-09-661-569-15
US-09-661-768A-33
US-09-019-793A-105
US-09-019-793A-105
US-09-019-793A-169
US-08-182-968A-168
US-08-182-968A-168
US-08-182-968A-169
US-08-174-306A-169
US-08-774-306A-169
US-09-044-156A-169
US-09-044-169
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US-09-04-164-169
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US-09-096-172-6
US-09-422-978-6
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Compugen Ltd
                                                                                                    Sequence 9, Appli
Sequence 15, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 168, App
Sequence 169, App
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Sequence
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Sequence
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Sequence
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Sequence 6, Appli
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                 20, Appli
4, Appli
1307, Ap
                                                                                                                                                                                                                                                                                                                                         6304, Ap
9775, Ap
                                                                                           Appli
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APPLICANT: Gilchrest, Barbara A.
APPLICANT: Gilchrest, Mark
APPLICANT: Gilchrest, Mark
ITTLE OF INVENTION: Use of Locally Applied D
FILE REFERENCE: BU94-68A2;
CURRENT APPLICATION UMMBER: US/09/048,927
CURRENT FILING DATE: 1998-03-26
EARLIER APPLICATION NUMBER: 08/952,697
EARLIER FILING DATE: 1996-06-03
EARLIER APPLICATION NUMBER: 08/467,012
EARLIER APPLICATION UMBER: 08/467,012
EARLIER FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 4
SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA; ORGANISM: Artificial Sequence; FEATURE: ; OTHER INFORMATION: DNA Fragment US-09-048-927-2
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                                                                                                                                                                                            US-09-096-172-6
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US-09-048-927-2
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Best Local S
Matches 9
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                                                                                                                                               Sequence 6, Application US/09096172
Patent No. 6284252
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09048927 Patent No. 6147056
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virgin:
                                                        APPLICANT: MEHTALI, Majid
APPLICANT: SORG, Tania
TITLE OF INVENTION: HEW TRANSDOMINANT TAT VARIANTS OF
TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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9; Conserv
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US-08-699-771B-4
US-08-606-505B-45
US-09-616-990-45
US-09-616-990-45
US-09-371-772B-53
US-09-371-772B-53
US-08-135-511-12
US-08-135-511-12
US-08-319-492B-735
US-08-320-559-9
US-08-327-392-9
US-08-187-453-12
US-08-77-412B-7
US-08-77-412B-7
US-08-98-77-412B-7
US-08-98-77-412B-7
US-08-98-98-77-412B-7
US-08-98-98-77-412B-7
US-08-98-98-77-412B-7
US-08-912-272-87
US-09-950-159-26
US-09-071-433-79
US-09-071-433-79
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Pred. No.
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45, Appli
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1958, Ap
503, Appl
12, Appl
13, Appl
14, Appl
16, Appl
26, Appl
27, Appl
28, Appl
29, Appl
39, Appl
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; SEQUENCE DESCRIPTION: SEQ ID NO: 20: US-10-232-927A-20

Query Match 100.0%; Score 11; DB 13; Length 16; Best Local Similarity 100.0%; Pred. No. 4.7e+03; Matches 11; Conservative 0; Mismatches 0; Indels

0; Gaps

0;

Search completed: January 1, 2004, 01:10:37 Job time : 129.241 secs

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; OTHER INFORMATION: Antisense sequence US-10-038-335-1
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                                          PRIOR APPLICATION NUMBER: PCT/US93/09297
PRIOR FILING DATE: 1993-09-29
PRIOR APPLICATION NUMBER: 07/954,185
PRIOR FILING DATE: 1992-09-29
                                                                                                                                                                  CURRENT FILING DATE: 2001-01-02
PRIOR APPLICATION NUMBER: 09/299,058
                                                                                                                                                                                                                    FILE REFERENCE: ISIS-4976
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ecker, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 07/954,185
PRIOR FILING DATE: 1992-09-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/038,335
                                                                                                                                                                                                                                          TITLE OF INVENTION: Modulation Of Telomere Length By Oligonucleotides Having A G-Cor
TITLE OF INVENTION: Sequence
                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/038,335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Modulation Of Telomere Length By Oligonucleotides Having A G-Cor
TITLE OF INVENTION: Sequence
FILE REFERENCE: ISIS-4976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                             APPLICANT:
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TYPE: DNA
ORGANISM: No. US20030096776A1el sequence
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Les 7; Conserv
                                                                                                                APPLICATION NUMBER: 08/403,888 FILING DATE: 1995-06-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/403,888
FILING DATE: 1995-06-12
APPLICATION NUMBER: PCT/US93/09297
FILING DATE: 1993-09-29
                                                                                                                                                   FILING DATE: 1999-04-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 09/299,058 FILING DATE: 1999-04-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
           PatentIn version 3.1
                                                                                                                                                                                                                                                                    Vickers, Time-
Chiang, Ming-yi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wyatt, Jacqueline
Bennett, C. Frank
Hanecak, Ronnie
Brown-Driver, Vickie
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No. US20030096776A1
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Bennett, C. Frank
Hanecak, Ronnie
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Chiang, Ming-yi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anderson,
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                                                                                                              1995-06-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    version 3.1
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4.7e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-232-927A-20/c
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GENERAL INFORMATION
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Best Local Similarity
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                                                                         TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: No. US20030096776A1el sequence
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                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                REFERENCE/DOCKET NUMBER: 224/232 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                   FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Chambers, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Michael D. West
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/378,535 FILING DATE: 20-Aug-1999
                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTTAGGGTTAG 11
                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/819,867
                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/10/232,927A
                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: IBM P.C. DOS
SOFTWARE: FastSEQ for Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/10232927A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homayoun Vaziri
INVENTION: THERAPY AND DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Nam Woo Kim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Michael
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Scott L. Weinrich
Catherine M. Strahl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jerry Shay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Suite 4700
                                                                                                            (213) 955-0440
                                                                                                                                 (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 11; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                            29-Aug-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                         storage
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h H. Blackburn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONDITIONS RELATED TO
TEOLOMERE LENGTH AND/OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELOMERASE ACTIVITY
                                                                                                                                                                                                   Daniel M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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Length 13;

Indels

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US-10-122-633-9/c
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                                                                                                                                                                                                                              US-09-893-252-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 9
LENGTH: 11
TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
                                SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/10122633 Publication No. US20030032611A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                            GENERAL INFORMATION
                                                                                                                                                                                        Sequence 4, Application US/09893252
Publication No. US20030012755A1
                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2001-03
                                                                                                          APPLICANT: Ahluwalia, Gurpreet S. TITLE OF INVENTION: REDUCTION OF FILE REFERENCE: 00216-552001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 0054.1088-019
CURRENT APPLICATION NUMBER: US/10/122,633
CURRENT FILING DATE: 2002-04-12
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                           NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
EQ ID NO 4
                                                                              CURRENT FILING DATE: 2001-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: PCT/US01/10162
PRIOR FILING DATE: 2001-03-30
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                                                                                                                                              APPLICANT: Styczynski, Peter
APPLICANT: Ahluwalia, Gurpro
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ORGANISM: Artificial Sequence
FEATURE:
 TYPE: RNA
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Local Similarity 100.0%;
les 11; Conservative
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Conservative
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US-10-368-451-1
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RESULT 13
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CURRENT FILING DATE: 203-01-21
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 13
TYPE: DNA
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Publication No. US20030186298A1
GENERAL INFORMATION:
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Best Local
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CURRENT FILING DATE: 2003-02-20
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TITLE OF INVENTION: Accelerator And Acceleration Method For Hybridization
                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: JP 2002-090129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: PH-1700
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TITLE OF INVENTION: POLYMER CHIP AND METHOD FOR IDENTIFYING AN IONIC POLYMER
                                                                                                                                                                                                                                          LENGTH: 13
TYPE: DNA
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Pred. No. 4.7e+03;
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                                                                                                                                                                                                                                 FILE REFERENCE: 0054.1088-018
CURRENT APPLICATION NUMBER: US/10/122,630
CURRENT FILING DATE: 2002-04-12
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APPLICANT: Eller, Mark S.
APPLICANT: Yaar, Mina
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                                   NUMBER OF SEQ I
                                                                                                                                                                                                 PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                      IITLE OF INVENTION: Method to Inhibit Cell Growth Using
IITLE OF INVENTION: Oligonucleotides
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NO
5
                                                   APPLICATION NUMBER: PCT/US01/10162 FILING DATE: 2001-03-30
                                                                                     APPLICATION NUMBER: US 09/540,843 FILING DATE: 2000-03-31
                                                                                                                         APPLICATION NUMBER: US 09/048,927 FILING DATE: 1998-03-26
                                                                                                                                                             APPLICATION NUMBER: PCT/US96/08386 FILING DATE: 1996-06-03
                                                                                                                                                                                                                APPLICATION NUMBER: US 08/467,012
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ETILING DATE: 07-Feb-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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               FastSEQ
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/057,351 FILING DATE: 08-APR-1994
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               for Windows Version 4.0
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(415) 576-0300
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Best Local :
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Publication No. US20030032611A1
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           PILE REFERENCE: 0054.1088-019
CURRENT APPLICATION NUMBER: US/10/122,633
CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: US 09/540,843
                                                              TITLE OF INVENTION: Method to Inhibit Cell Growth Using TITLE OF INVENTION: Oligonucleotides FILE REFERENCE: 0054.1088-019
                                                                                                                                  APPLICANT: Gilchrest,
APPLICANT: Eller, Mai
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PRIOR FILING DATE: 20
NUMBER OF SEQ ID NOS:
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PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: US 09/540,843
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APPLICANT: Eller, Mar
APPLICANT: Yaar, Min
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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Yaar, Mina
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Yaar, Mina
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2001-03-30
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Publication No. US20030138814A1
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SEQ ID NO 63
LENGTH: 11
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Sequence 63, Application US/09835370
Publication No. US20030022172A1
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                                                        APPLICANT: Gryaznov, Sergei
APPLICANT: Pongracz, Krisztina
APPLICANT: Tolman, Richard L.
APPLICANT: Morin, Gregg B.
TITLE OF INVENTION: Oligonucleotide Conjugates
FILE REFERENCE: 072/002P
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: UHLMANN, EUGEN
APPLICANT: BREIPOHL, GERHARD
APPLICANT: WILL, DAVID W
TITLE OF INVENTION: POLYAMIDE NUCLEIC ACID DERIVATIVES AND AGENTS AND
TITLE OF INVENTION: PROCESSES FOR PREPARING THEM
FILE REFERENCE: 02481.1742 SEQUENCE LISTING
CURRENT APPLICATION NUMBER: US/09/835,370
CURRENT FILING DATE: 2001-04-17
               CURRENT APPLICATION NUMBER: US/10/255,535
CURRENT FILING DATE: 2002-09-25
PRIOR APPLICATION NUMBER: PCT/US02/09138
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                  APPLICANT: Geron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: nucleotic OTHER INFORMATION: base sequence of PNA derivatives that bind to OTHER INFORMATION: viral and cellular targets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                                    Sequence 2, Application US/10359935 Publication No. US20030153076A1 GENERAL INFORMATION:
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CURRENT FILLING DATE: 2002-09-25
PRIOR APPLICATION NUMBER: PCT/US02/09138
PRIOR FILING DATE: 2002-03-21
PRIOR APPLICATION NUMBER: US 60/278,322
PRIOR FILLING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 19
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SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Oligonucleotide Conjugates
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ORGANISM: Artificial Sequence
FEATURE:
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                                               CORRESPONDENCE ADDRESS
                                                                                 Andrews, William H. TITLE OF INVENTION: Mammalian
                                                                                                                                                    APPLICANT: Villeponteau,
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Pongracz, Krisztina
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Morin, Gregg B.
CITY: San Francisco
                 ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
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No. US20030138814A1
                                                                   OF SEQUENCES:
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Funk, Walter
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/US09D_NEW_PUB.seq:*

13: /cgn2_6/ptodata/1/pubpna/US09D_NEW_PUB.seq:*

14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

17: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

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18: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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US-110-129-630-5
US-110-122-630-9
US-110-122-633-9
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Patent No. US20010034439A1
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Tele
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Ver

CURRENT APPLICATION DATA:

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FILING DATE: 08-APR-1994

CLASSIFICATION DATA:

APPLICATION NUMBER: US 08/272,102

FILING DATE: 07-JUL-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/330,123

APPLICATION NUMBER: US 08/330,123

FILING DATE: 07-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/330,123

FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/472,802

FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/472,802
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CITY: San Francisco
STATE: California
COUNTRY: USA
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US-10-32-927A-24
US-10-232-927A-24
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